

FIGURE 1

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTACAAAAGGTGCAGGTATG
AGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGT
TTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAAATTTGGACATCTGCTGCTTTCATATTT
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG
TACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGGCAGTTTATGCATTG
CTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCTGAAGAGAACGTTATCATCAA
TTAAACAAGGCTGGCCTTGTACTTGAATACTGAGTTGTTTAGGACTTTCTATTGTGGCAAACCTT
CCAGAAAACAACCCTTTTTGCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCAT
TATATATGTTTGTTCAGACCATCCTTTCTACCAAATGCAGCCCAAAATCCATGGCAAACAAGTC
TTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTTAGCATGCTGACTTGCTC
ATCAGTTTTGCACAGTGGCAATTTTGGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGG
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTT
GGTTTTTTCCTGACTTACATTCGTGATTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACA
TGGATTAACCCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCA
GAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG
TTCACAGAAGTTGCTTATTCTTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACT
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATCTAAAGGATATCAT
CAAGAAGACTATTAAAAACACCTATGCCTATACCTTTTTTATCTCAGAAAATAAAGTCAAAGACT
ATG

FIGURE 2

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV
LCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG
MGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW
NPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR
LLSRDI

Important features:

Type II transmembrane domain:

amino acids 13-33

Other Transmembrane domains:

amino acids 54-73, 94-113, 160-180, 122-141

N-myristoylation sites.

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCC GGCTGCAGCACCTGGGAGAAGGCAGACC
GTGTGAGGGGGCCTGTGCCCCAGCGTGTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTC
CTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTG
GATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAG
GTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATCTTTGAAATCTTAGG
AGTATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGG
TTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAAACAACGA
CTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCC
CATCTCAGCCCAAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTTGGTGTGATTGGAG
TGACTCTCATGGCTCTTCTTTCTGGATTGGTGTCTCAACTGCCCATACACTTACATGTCTTACTTC
CTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT
CATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACA
AACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGGAAGTGAATCTTACT
CTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTTCTGGAACAGCTGATCT
ATATGCTACCAAGGAGAGAATAGAACTCCAAACCTTCAAGGGGAAATATTTAATTTTCTTGGTT
ACTTTTTCTCTATTTACTGTGTTTGGAAAATTTTCATGGCTACCATCAATATTGTTTTTGATCGAGTT
GGGAAAACGGATCCTGTCAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGT
GAAGTTTGGTCCCAACACATTTCTTCATTCTTGTGGAATAATCATCGTCACATCCATCAGAGGAT
TGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCTCCAATGTCATTGTCCTG
CTATTAGCACAGATAATGGGCATGTACTTTGTCTCTCTGTGCTGCTGATCCGAATGAGTATGCCTTT
AGAATACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGTTTG
ATGTGATCTTCTGGTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAACAGGCACCA
GAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAAATTTA
GATATAAGAGGGGGGAAAAATGGAACAGGGCCTGACATTTTATAAACAAACAAAATGCTATGGTAGC
ATTTTTCACCTTCATAGCATACTCCTTCCCCGTCAGGTGATACTATGACCATGAGTAGCATCAGCCAG
AACATGAGAGGGGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGG
TGTAGAGGCGGAGAGGAGCCAAGAACTAAAGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGT
CTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTAAGGTTACATGGAAAAGGTTATAGCTTTG
CCTTGAGATTGACTCATTAATAATCAGAGACTGTAACAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCG
ACTCTAGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTATTGCAGCTTATAATG

FIGURE 4

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEILGV
LNSSSRYPFHWMNLCVILLILVFMVPPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFFWKLGBP
FPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERLLQ
TMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQQEVDLEELSRQ
LLETADLYATKERIEYSKTFKGKYNFLGYFFSIYCVWKIFMATINIVFDRVGKTDVTRGIEI
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLAQIMGY
FVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSALSSILFLYLAHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

FIGURE 5

AGCAGGGAAATCCGGATGTCTCGGTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCC
 AGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGT
 GTTCCCTGGCTCTGAAGGGGTAGGCACGATGCGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT
 TCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGT
 GTCATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAG
 AAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCC
 TTGAAAGCTAGCTTTGAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTCTAG
 GATTAGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTGGAAGGTTCCAGTGA
 GCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATTCCAGAA
 ATTATCACCACCAAAGATCCCATATTCAACACTCAAACGACAAACAACAGAATTTATTGT
 CAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACATACCTGCCCTACTACTACTCTC
 CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTGTGTGCACAGAAGTTTTATG
 GAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAAGAATGA
 AGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTCTGCTCTCTCTCTCTCTCTCTCTG
 CAGCTGGTCTTGGATTTTGTCTATGTCAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAT
 CAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAA
 TGAGGAATCAAAGAAAACCTGATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGC
 GATGCTCGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTT
 CATGCTCCTTACCCTGCCCGAGCTGGGGAAATCAAAGGGCCAAAGAACCAAAGAAGAAAGTCCA
 CCCTTGGTTCCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAAT
 GCCCTTCTCCTTATTGTAACCCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCCT
 TTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTGTCAAAGTGAAGGAC
 CTAAACATCTCATCAGTATCCAGTGGTAAAGGCTCCTGGCTGTCTGAGGCTAGGTGGGTG
 AAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGACCCCTTCTCA
 GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTGAGCCCGGTAAGAGCAAAAGAAT
 GGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAA
 GCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTCAGCAGGGACTGTAAC
 ACAGACAGGGTCAAAGTGTCTTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACA
 CTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCTAGGAAATATACTTTTACAAGTAACA
 AAAATAAAAACCTTATAAATTTCTATTTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATT
 ACTCAGTAATTTGTTTAAAAAGTAATAAATTCACAAACATTTGCTGAATAGCTACTATATGTC
 AAGTGCTGTGCAAGGTATTACACTCTGTAATTGAATATTATTCCTCAAAAAATTGCACATAGTAG
 AACGCTATCTGGGAAGCTATTTTTTTCAGTTTTGATATTTCTAGCTTATCTACTTCCAAACTAAT
 TTTTATTTTTGCTGAGACTAATCTTATTCATTTCTCTAATATGGCAACCATTATAACCTTAATT
 TATTATTAACATACCTAAGAAGTACATTGTTACCTCTATATACCAAGCACATTTTAAAAGTGCC
 ATTAACAAATGTATCACTAGCCCTCCTTTTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATT
 TGTGACAAAAAATTAAAGCATTTAGAAAACCTT

FIGURE 6

MARCFSLVLLLTISIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLG
LSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYN
SSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR
RKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGFGVPTALLVLALLFFGAAAGLGFCYVK
RYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNNEESKKTDKNPPEESKSPSKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 7

CGCCGCGCTCCCGCACCCGCGGCCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGAGCCCGGC
GGCCTCCCGCGGGGAGCGAGCAGATCCAGTCCGCGCCGAGCGCAACTCGGTCCAGTCGGGGCGG
CGGCTGCGGGCGCAGAGCGGAGATGAGCGGGCTTGGGGCCACCCTGCTGTGCCTGCTGCTGGCGG
CGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTCAAGCCCGGCCCG
GCTCTCAGTACCCGCGAGGAGGAGGCCACCTCAATGAGATGTTCCGCGAGGTTGAGGAAGTAT
GGAGGACACGCGAGCACAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTA
AAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCAGCTATCACAATGAGACCAACACAGAC
ACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAATTCACAAGATAACCAACAACAGAC
TGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTGTGGGAGACGAAGAAGGCAGAAGGAGCC
ACGAGTGCATCATCGACGAGGACTGTGGGCCCCAGCATGTACTGCCAGTTTGCCAGCTTCCAGTAC
ACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAGTGTGTGGAGACCA
GCTGTGTGTCTGGGGTCACTGCACCAAAATGGCCACCAGGGGCAGCAATGGGACCATCTGTGACA
ACCAGAGGACTGCCAGCCGGGGCTGTGCTGTGCCTTCCAGAGAGGCTGCTGTTCCCTGTGTGC
ACACCCCTGCCCGTGGAGGGCGAGCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCAC
CTGGGAGCTAGAGCCTGATGGAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGC
CCCACAGCCACAGCCTGGTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGG
GAGATCCTGCTGCCCAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCG
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTG
CCGCCGCTGCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAA
TAGAAATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCTA
CATCTTCTTCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTACAGCT
CCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGTCTGGGAGAGTCAGGCAGGGTTAAACTGCA
GGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAGACAGCCG
TTTGTCTACATGGCTTTGATAATTGTTTGGGGGAGGAGATGGAACAATGTGGAGTCTCCCTC
TGATTGGTTTTGGGGAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAACCTGGCAAAAATG
CAACAAATGAATTTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTTGC
AGATGAAATGTTCTGTTTCCCTGCAATTACATGTGTTTATTCATCCAGCAGTGTGCTCAGCTCC
TACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATTCCCTCTCTCAGCACAGCCTGGGG
AGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCC
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCATCTGGTTGTGACTCTAAGCTCAGTGTCTCT
CTCCACTACCCACACAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAAGGAAGGAGAATGGGAT
TTTTCTTGAGGCATGCACATCTGGAATTAAGGTCAAATAATTCTCACATCCCTCTAAAAGTAAA
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGAT
ATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACCTTTGAAAGGTATATGACTGAGCGTAGCA
TACAGGTTAACCTGCAGAAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGC
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGC
TGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATG
TTTTCAGGTGTCATGGACTGTTGCCACCATGTATTCATCCAGAGTTCTTAAAGTTTAAAGTTGCA
CATGATTGTATAAGCATGCTTTCTTTGAGTTTTTAAATTATGTATAAACATAAGTTGCATTTAGAA
ATCAAGCATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 8

MQRLGATLLCLLLAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQHKL
RSAVEEMEAEEAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTGQMFSE
TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQMLCTRDSECCGDQLCVWGHC
TKMATRGSNGTICDNQRDCQPLCCAFQRGLLFPVCTPLPVEGELCHDPASRLLDLITWELEPDG
ALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSFMEEVRQELEDLE
RSLTEEMALGEPAAAAAALLGGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 9

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCCAC
GGCCACCTTGTGAACCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCATCAAAG
GCCTAATCCAACGTTCTGTCTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTCTGGACCCTT
AACTGGGTACTGGCCCTGGGCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTTCTACTGGGCCTT
CCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCCGCACACTCCGTTACC
ACACTGGGTCATTGGCATTGGAGCCCTCATCCTGACCCTTGTGCAGATAGCCCGGGTCATCTTG
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGCCCGCTGCATCATGTGCTGTTT
CAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCCATAACCGCAATGCATACATCATGA
TCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAAAATGCGTTTCATGCTACTCATGCGAAAC
ATTGTCAGGGTGGTCTGCTGGACAAAGTACAGACCTGCTGCTGTTCTTTGGGAAGCTGCTGGT
GGTCGGAGGCGTGGGGTCTGTCTTCTTTTTTTCTCCGGTCGCATCCCGGGCTGGGTAAAG
ACTTTAAGAGCCCCACCTCAACTATTACTGGCTGCCATCATGACCTCCATCCTGGGGGCCTAT
GTCATCGCCAGCGGCTTCTTCAGCGTTTTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCCT
GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAA
AGATTCTGGGCAAGAAGAACGAGGCGCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGG
CCCTGATCCAGGACTGCACCCACCCACCCTCCAGCCATCCAACCTCACTTCGCCTTACAGGT
CTCCATTTTGTGGTAAAAAAGTTTTAGGCCAGGCGCGTGGCTCACGCCTGTAATCCAACACT
TTGAGAGGCTGAGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTG
AAACCTCCGTCTCTATTAATAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCA
GCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGA
GATCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAACAA
AAGATTTTATTAAAGATATTTTGTAACTC

FIGURE 10

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLEFWTL
NWVLALGQCVLGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAKNAFMLLMRN
IVRVVVLDDKVTDLFFFGLLVVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY
VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYSKSLKILGKKNEAPPDNKKRKK

Important features:

Transmembrane domains:

amino acids 57-80 (type II), 110-126, 215-231, 254-274

N-glycosylation sites.

amino acids 16-20, 27-31, 289-293

Hypothetical YBR002c family proteins.

amino acids 276-288

Ammonium transporters proteins.

amino acids 204-231

N-myristoylation sites.

amino acids 60-66, 78-84

Amidation site.

amino acids 306-310

FIGURE 11

GCCCCGCGCCCCGGCGCGGGCGCCCCGAAGCCGGGAGCCACCGCCATGGGGGCGCTGCCTGGGAGCCTGC
TCCCTGCTCAGCTGCGCGTCTGCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGCTGCTGCCCCGC
CAGCCGCAACTCCACCGTGAGCCGCCCTCATCTTCACGTTCTTCTCTTCTGGGGGTGCTGGTGTCCA
TCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTGCCCTGGGTGTGTGAGGAGGGGGCC
GGGATCCCCACCGTCTGCGAGGGCCACATCGACTGTGGCTCCCTGGCTTGGCTACCGCGCTGTCTACCG
CATGTGCTTCGCCACGGCGGCTTCTTCTTCTTCTTTTTCACCCTGCTCATGCTCTGCGTGAGCAGCA
GCCGGGACCCCCGGGTGCCATCCAGAATGGGTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCGCTC
ACCGTGGGTGCCTTCTACATCCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGCTCGTGGG
CTCCTTCTCTTTCATCCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCCTGGAACAGCGGT
GGCTGGGCAAGGCCGAGGAGTGCATTCCCGTGCCTGGTACGCAAGGCCTCTTCTTCTTCACTCTCCTC
TTCTACTTGCTGTGATCGCGGCGTGGCGCTGATGTTTCATGTACTACACTGAGCCAGCGGCTGCCA
CGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGCCATCGCTGCTGTCTGCTG
CCAAGGTCCAGGACGCCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTATCACCTCTACACCATG
TTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTTGCCAACCCAGCT
GGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAGACCCAGTGGTGGGATGCCCCGAGCATTG
TGGGCTCATCATCTTCTCTGTGCACCTCTTCATCAGTCTGCGCTCCTCAGACCACCGGCAGGTG
AACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCACACAGCAGCAGCAGCAGGAGT
GGCAGCCTGTGAGGGCCGGGCTTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCC
ACTTCTGCCTGGTGTGCTGGCCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCGGTGAG
ACCCGGAAGATGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCT
CCTCTACCTGTGGACCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTGAGGCAGCCTCA
CAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTC
CCCACACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTGCCCTGAGCCGGGC
CTTCTAGTCGTAGTGCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCAC
ACCCACACGGTGGAGCTGCCTCTTCTTCCCCCTCCTCCTGTTGCCATACTCAGCATCTCGGATGAA
AGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGGCTGCTGGAGAGAGCGGGGAACCTCCCACCACAG
TGGGGCATCCGGCACTGAAGCCCTGGTGTCTGCTGACGTCCCCCAGGGGACCCCTGCCCCCTTCTGT
GACTTCGTGCCTTACTGAGTCTCTAAGACTTTTCTAATAACAAGCCAGTGCCTGTAAAAAAA

FIGURE 12

MGACLGACSLSCASCSCGAPCILSCCPASRNSTVSRLIFTFFFLGVLVSIIMLSPGVESQL
YKLPWVCEEAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFTLLMLCVSSSRDPRAAIQ
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFILIQLVLLIDFAHSWNQRWLKAE
ECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVVSIAAVLPKV
QDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI
VGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQVAAACEGRAFDNEQDGVITYSY
SFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVWKICASWAGLLLYLWTLVAPLLLRNRD
FS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 13

CGGGCCAGCCTGGGGCGGCCGAGGAACCAACCGTTAAGGTGTCTTCTCTTTAGGGATGGTGA
GGTTGAAAAAGACTCCTGTAACCCCTCCTCCAGGATGAACCACTGCCAGAAGACATGGAGAACG
CTCTCACCAGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCATCAACCCACACAA
CTCATGGCCAGGATTGAGTCCTATGAAGGAAGGAAAAGAAAGGCATATCTGATGTCAGGAGGAC
TTTCTGTTTGTGTTGTCACCTTTGACCTCTTATTCGTAACATTACTGTGGATAATAGAGTTAAATG
TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTACTATTCTTCATAT
TTTGATATATTTCTTCTGGCAGTTTTTCGATTAAAGTGTAAATACTTGCATATGCTGTGTGCAG
ACTGCCCATTTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAAGTGCCTTTTTACTAGCAAAAG
TGATCCTTTTCGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTGCCCATCATTTTCATTCATC
CTTGCTGGATTGAGACGTGGTTCTGGATTTCAAAGTGTTACCTCAAGAAGCAGAAGAAGAAAA
CAGACTCCTGATAGTTCAGGATGCTTCAGAGAGGGCAGCACTTATACCTGGTGGTCTTTCTGATG
GTCAGTTTTATTCCCTCCTGAATCCGAAGCAGGATCTGAAGAAGCTGAAGAAAAACAGGACAGT
GAGAAACCACTTTTAGAACTATGAGTACTACTTTTGTTAAATGTGAAAAACCTCACAGAAAGTC
ATCGAGGCAAAAAGAGGCAGGCAGTGAGTCTCCCTGTGCGACAGTAAAGTTGAAATGGTGACGTC
CACTGCTGGCTTTATTGAACAGCTAATAAAGATTTATTTATTGTAATACCTCACAAACGTTGTAC
CATATCCATGCACATTTAGTTGCCTGCCTGTGGCTGGTAAGGTAATGTCATGATTCATCCTCTCT
TCAGTGAGACTGAGCCTGATGTGTTAACAAATAGGTGAAGAAAGTCTTGTGCTGTATTCCTAATC
AAAAGACTTAATATATTGAAGTAACACTTTTTTAGTAAGCAAGATACTTTTTATTTCATTCAC
AGAATGGAATTTTTTTGTTTCATGTCTCAGATTTATTTTGTATTTCTTTTTTAACACTCTACATT
TCCCTTGTTTTTTAACTCATGCACATGTGCTCTTTGTACAGTTTTTAAAAGTGTAATAAAATCTG
ACATGTCAATGTGGCTAGTTTTATTTTCTTGTTTTGCATTATGTGTATGGCCTGAAGTGTGGA
CTTGCAAAAGGGGAAGAAAGGAATTGCGAATACATGTAAAATGTCACCAGACATTTGTATTATTT
TTATCATGAAATCATGTTTTTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGC
ACAAAATGACTTAAACCATTATATCATGTTTCCTTTGCGTTCAGCCAATTTCAATTAAATGAA
CTAAATTAAAAA

FIGURE 14

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRFTCLFVTFDLLF
VTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT
AVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLQPQEAEEENRLLIVQDASER
AALIPGGLSDGQFYSPPESEAGSEEAEKQDSEKPLLEL

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domains:

amino acids 54-72, 100-118, 130-144, 146-166

N-myristoylation sites.

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

FIGURE 15

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGACTGAGG
CCGCGGCCTGCCCCGCGCGCTCCCTGCGCCGCGCGCCCTCCCGGGACAGAAGATGTGCTCCAG
GGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCCAGGGCTGCCCAT
CCGGCTGCCAGTGCCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGGACCACGGTGCCC
CGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGC
AGGCAGCTTTGCCGGCCTGCCGGGCTGCAGCTCCTGGACCTGTACAGAACCCAGATCGCCAGCC
TGCCAGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTGGACCTGACGGCCAACAGGCTG
CATGAAATCACCAATGAGACCTTCCGTGGCCTGCGGCGCCTCGAGCGCCTTACCTGGGCAAGAA
CCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGCTCGACCGCCTCCTGGAGCTCAAGCTGC
AGGACAACGAGCTGCCGGGCACTGCCCCGCTGCGCCTGCCCGCCTGCTGCTGCTGGACCTCAGC
CACAAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAGGGCTGCGGCT
GGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACC
TGGATGTGTCCGACAACCACTGGAGCGAGTGCCACCTGTGATCCGAGGCCCTCCGGGGCTGACG
CGCCTGCGGGCTGGCCCGGCAACACCCGCTTGGCCAGCTGCGGCCCGAGGACCTGGCCGGCTGGC
TGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCC
TCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGC
TGGTTTGGCCCTGGGTGCGCGAGAGCCACGTCACTGGCCAGCCCTGAGGAGACGCGCTGCCA
CTTCCCGCCCAAGAAGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCAG
CCACCACCACACAGCCACAGTGCCACCACGAGGCCGCTGGTGCGGGAGCCACAGCCTGTCT
TCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCAGCCCGCCCTC
CACTGCCCCACCGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCA
ATGGGGGCACATGCCACCTGGGGACACGGCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACG
GGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCGAG
GCCACCACGGTCCCTGACCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGC
AGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCG
GGCCCTGATAAGCGGCTGGTGACGTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCA
GCTGCGGGCCCAACGCCACTTACTCCGTCTGTGTCTATGCCTTTGGGGCCCGGGCGGGTGCCGGAGG
GCGAGGAGGCTGCGGGGAGGCCATACACCCAGCCGTCCACTCCAACCACGCCCCAGTCACC
CAGGCCCCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGC
GCTGGCTGCGGTGGGGGAGCCTACTGTGTGCGCGGGGGCGGCCATGGCAGCAGCGGCTCAGG
ACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCCCTGGAAGTGGAGGGAGTGAAGGTCCCCTTGGAG
CCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGCTGTAGTGTGAGGTGCC
ACTCATGGGCTTCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAAAAGCCCTACATCTAAAGCCA
GAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCC
ACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCT
GGGCCCTGTTCCTCTGGACCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCC
CTAACGTCCCCAGAACCAGTGCCATATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTC
CCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCTGCTGGGCTCTCCAC
TCCAGGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGC
GGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGC
TTTAGGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATTCT
GGGAAGATGTTTTCAAACCTCAGAGACAAGGACTTGGTTTTTGTAAAGACAAACGATGATATGAA
GGCCTTTTGTAAAGAAAAATAAAAGATGAAGTGTGAAA

FIGURE 16

MCSRVPLLLLLLLLLALGPGVQGCPSGCQCSQPQTTFCTARQGTTPRDVPPDTPVGLYVFENGIT
MLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLRRLERLY
LGKNRIRHIQPGAFDTLDRILLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEPGILDTANVE
ALRLAGLGLQLDEGLFSRLRNLDLVDSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDL
AGLAALQELDVSNSLSLQALPGDLSGLFPRLRLAAARNPFNCVPLSWFGPWVRESHVTLASPEE
TRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAP
SPPSTAPPTVGPVPQPDQCPPSTCLNGGTCHLGRHHLACLCEGFTGLYCESQMGQGRPSPTP
VTPRPPSLTLGIEPVSPTSRLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEY
TVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAV
LLAALAAVGAAYCVRGRAMAAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGGEALPSGSE
CEVPLMGFPGLQSPHAKPYI

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 579-599

EGF-like domain cysteine pattern signature.

amino acids 430-442

Leucine zipper pattern.

amino acids 197-219, 269-291

N-glycosylation sites.

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

Tyrosine kinase phosphorylation sites.

amino acids 124-131, 337-345

N-myristoylation sites.

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,
594-600, 640-646

FIGURE 17

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCATGCG
GGTCCGGATAGGGCTGACGCTGCTGCTGTGTGCGGTGCTGCTGAGCTTGGCCTCGGCGTCCTCGG
ATGAAGAAGGCAGCCAGGATGAATCCTTAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTA
AAGGACCATACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTTCTTGATTAGAAGAATCTGA
ATTAGAATCCTCTATTCAAGAAGAGGAAGACAGCCTCAAGAGCCAAGAGGGGGAAAGTGTACAG
AAGATATCAGCTTTCTAGAGTCTCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTA
CGGAAACCAGCTTTGACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCT
TTTCCTAGATAAGGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGCCAGACTGTGGTGTG
CTACAACCTATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAACTGAAGAAGAGGCTGCT
AAGAGACGGCAGATGCAGGAAGCAGAAATGATGTATCAAATGGAATGAAATCCTTAATGGAAG
CAATAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA
CCAAAGCCCTGGAGAGAGTGTCTATGCTCTTTTATTTGGTGATTACTTGCCACAGAATATCCAG
GCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGCTCTTGG
CTTTCTGTATGCCTCTGGACTTGGTGTTAATTCAAGTCAGGCAAAGGCTCTTGATATTATACAT
TTGGAGCTCTTGGGGCAATCTAATAGCCACATGGTTTTTGGTAAGTAGACTTTTAGTGGAAGGCT
AATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACCTTTTCAGCTTTTCATGATC
CAGATTTGCTTGTTAATAGACCAAATATTCAGTTGAACTTCCTTCAAATCTTGTTAATGGATAT
AACACATGGAATCTACATGTAAATGAAAGTTGGTGGAGTCCACAATTTTTCTTTAAATGATTAG
TTTGGCTGATTGCCCCATAAAAGAGAGATCTGATAAATGGCTCTTTTAAATTTTCTCTGAGTTG
GAATTGTCAGAATCATTTTTTACATTAGATTATCATAATTTTAAAAATTTTCTTTAGTTTTTCA
AAATTTTGTAATGGTGGCTATAGAAAAACAACATGAAATATTATACAATATTTGCAACAATGC
CCTAAGAATTGTTAAATTCATGGAGTTATTTGTGCAGAATGACTCCAGAGAGCTCTACTTTCTG
TTTTTTACTTTTCATGATTGGCTGTCTTCCATTTATTCTGGTCATTTATTGCTAGTGACACTGT
GCCTGCTTCCAGTAGTCTCATTTTCCCTATTTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGG
AAGATTAACTCATTTTTAATAAAATTATGTCTAAGATTAAAAA
AAA

FIGURE 18

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLDSESESEL
ESSIQEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHGEPCHFPFLFLDK
EYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEEAAKRRQMGEAEMMYQTGMKILNGSNKKSQKR
EAYRYLQKAASMNHTKALERSYALLFGDYLPQNIQAAREMFEKLTEEGSPKGQTALGFLYASGLGVN
SSQAKALVYYTFGALGGNLIAMVLVSRL

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 195-199, 217-221, 272-276

Tyrosine kinase phosphorylation site.

amino acids 220-228

N-myristoylation sites.

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

Glycosaminoglycan attachment site.

amino acids 267-271

Microbodies C-terminal targeting signal.

amino acids 299-303

Type II fibronectin collagen-binding domain protein.

amino acids 127-169

Fructose-bisphosphate aldolase class-II protein.

amino acids 101-119

FIGURE 19

AATTCAGATTTTAAAGCCCATCTGTCAGTGAATTTTCATGAACTAGCAAGAGGACACCATCTTCTT
GTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGAAAAATGCTCTTTTGGGTGCTAGG
CCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAGACATCACTG
ATAAGTACATTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCCAGAACTTTTGAT
AAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAACAGCTTTAAAGGCAGA
AACCTCAGAGAGACTTCGTAATGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG
CCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGTCTGATCAATAATGCTGGTGT
CCCGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA
CCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAG
TTATTAATGTCTCCAGTGTTGGAGGTGCGCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAA
TATGCAGTGAAGGTTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTC
ATGCATTGAACCAGGATTGTTCAAAACAACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAC
TCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAACAACAATATGGAGAAGGTTACATTGAAAAA
AGTCTAGACAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTG
CATGGACCACGCTCTAACAAGTCTCTCCCTAAGACTCATTATGCCGCTGAAAAGATGCCAAA
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAA
GCAGAGCTGGCTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGA
AATTGGCCGATTTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACT
CATTTAGATCGTGCTTATTTGGATTGCAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGT
CCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCTTGCCCT
GTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATGA
TCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTACAGTAACCTTGTGAATGTTAAGT
ATCATCTCTTATCTAAATATTAAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 20

MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESG
STALKAETSERLRTVLLDVTDPENVKRTAQWVKNOVGEKGLWGLINNAGVPGVLAPTDWLTLEDY
REPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDSLRRDMK
AFGVHVSCIEPGLFKNLADPVKVEKKLAIWEQLSPDIKQQYGEGYIEKSLDKLKGKNSYVNMD
LSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQKAELANPKAV

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 21

CTGAGGCGGCGGTAGCATGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGGCG
CACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAAGTAAAA
GGTGAAGCCAAGAACAGCATTACTGATTCCCAATGGATGATGTTGAAGTTGTTTATACAATTGA
CATTAGAAATATATTCATGCTATCAGCTTTTAGCTTTTATAATTCTTCAGGCGAAGTAAATG
AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATCCGT
CGTCATTAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACCTGCAGGAGCATT
TTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTCTACTC
ATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTTTTTACAGGGTACCTTTAGTGGTT
GCCAATCTGGGCATGTCTGAACAACTGGGTTATAAACTGTATCAGGTTCTGTATGTCCACTGG
TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTTGAAGAAGATGGATCCTTAAAGGAGG
TACATAAGATAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAAGTG
GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAAACAGATTAAACGAGAAATTGA
GAAAAGGAGAGGAGCACAGATTCAGGCAGCAAGAGAGAAGAACATCCAAAAGACCCTCAGGAGA
ACATTTTTCTTTGTGTCAGGCATTACGGACCTTTTTTCCAAATCTGAATTTCTTCATTATGTGTT
ATGTCTTTAAAAAATAGACATGTTTCTAAAGTAGCTGTAACCTACAACCACCATCTCGATGTAGT
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCAC
AAATCATTAAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTA
GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAT
GAGCAGCCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTC
CTACATTTTGATCCTTTTAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAAC
ATTTCTATTGTTTTTACTATGTTGAGCTACTGCAGTAAGTTCATTTGTTTTTACTATGTTACC
TGTTTGAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAACATCA
GATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCACTAAGTTGTTGAGGGGAAGGCTTACACAG
ACACATTCTTTAGAATTGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACT
TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATT
GAGACCATGTCTATTAAAAAATAAAATGAAAAGCAAGAATAGCCTTATTTTCAAATATGGAAA
GAAATTTATATGAAAATTTATCTGAGTCATTAAATTTCTCCTTAAGTGATACTTTTTTAGAAGTA
CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATCT
AAAATTTAAAAA

FIGURE 22

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLGGEVKGEAKNSITDSQMDDVEVVYTIDIQYI
PCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQDL
VFLLLTPSIITESCSTHRLEHSLYKPKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAV
QTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA
QIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCNYNHHLDDVVDNLTL
MVEHTDIPEASPASTPQIIKHKALDLDLRWQFKRSRLLDTDKRSKANTGSSNQDKASKMSSPET
DEEIEKMKGFGEYSRSPTF

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation sites.

amino acids 75-79, 322-326

N-myristoylation site.

amino acids 184-154

Growth factor and cytokines receptors family.

amino acids 134-150

FIGURE 23

GGCACAGCCCGCGGGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGAGCAGCGGACCAGCGCAGGGCAGCCAA
GCAGCGCGCAGCGAACCGCCGCCGCCACACCCCTCTGCGGTCCCCGCGGCGCTGCCACCCTTCCCTCCTTCCCC
GCGTCCCCGCTCGCCGGCCAGTCAGCTTGCCGGGTTGCTGCCCGCGAAACCCGAGGTACCCAGCCCGCGCTCT
GCTTCCCTGGCGCGCGCCGCTCCACGCCCTCCTTCTCCCTGGCCCGCGCTGGCACCAGGGGACCGTTGCTGA
CGCGAGGCCAGCTCTACTTTTCGCCCGCGCTCTCCTCCGCTGCTCGCTCTTCCACCAACTCCAACCTCCTTCCCC
TCCAGTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCGCTGCCGTAGCGCGCTTCCCGTCCGCTCCCAA
GGTGGGAACGCGTCCGCCCGGCCCGCACCATGGCACGGTTCGGCTTGCCCGCGCTTCTCTGCACCCTGGCAGTGCTC
AGCGCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCGACGTCTTTACGTGTCAAAGGCTTC
AACAGAACGATGCCCCCTCCACGAGATCAACGGTGATCATTTGAAGATCTGTCCCCAGGGTTCTACCTGCTGCTCT
CAAGAGATGGAGGAGAAGTACAGCTGCAAAAGTAAAGATGATTTCAAAGTGTGGTCAGCGAACAGTGCAATCATTTG
CAAGCTGTCTTTGCTTACGTTACAAGAAGTTTGATGAATCTTCAAAGAACTACTTGAAATGCAGAGAAATCCCTG
AATGATATGTTTGTGAAGACATATGCCATTTATACATGCAAAATCTGAGCTATTTAAAGATCTCTTCGTAGAGTTG
AAACGTTACTACGTGGTGGGAATGTGAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCTCCTGGAGCGGATG
TTCGCTGCTGTAACCTCCAGTACCCTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAG
CCCTTCGGAGATGTCCCTCGCAAATGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCGCTACTTTCTGCTCAAGGC
TTAGCGGTTGCGGGAGATGTGCTGAGCAAGGTCTCCGTGTTAAACCCACAGCCAGGTGTACCCATGCCCTGTTGAAG
ATGATCTACTGCTCCCACTGCCGGGCTCTCGTACTGTGAAGCCATGTTACAACCTACTGCTCAAACATCATGAGAGGC
TGTTTGCCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTA
GAGGGTCTTTCAACATTGAATCGGTGATGATCCCATGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGAT
AATAGTGTCAAGTGTCTCAGAAGGTTTTCCAGGGATGTGGACCCCAAGCCCTCCAGCTGGACGAATTTCTCGT
TCCATCTCTGAAAGTGCCTTCAGTGCTCGCTTCAGACCACATCACCCCGAGGAACGCCCAACCACAGCAGCTGGCACT
AGTTTGACCGACTGGTTACTGATGTCAAGGAGAACTGAACAGGCCAAGAAATCTGGTCCCTCCCTCCGAGCAAC
GTTTGCAACGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTAC
CTGTTTGCACTGACAGGAAATGGATTAGCCAACCAGGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAACCCAGAC
ATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG
GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGAAGTGGCTGTGAGTATCAGCAGTGCCCTTCAGAG
TTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGCTGGTGTCCGCTCTGGGGCA
CAGGCCTACCTCCTCACTGTCTTCTGCATCTTGTTCTGCTGTTATGCAGAGAGTGGAGATTAATTCTCAAACCTCTGAG
AAAAAGTGTTCATCAAAAAGTTAAAGGCACCAAGTTATCACTTTTCTACCATCCTAGTGACTTTGCTTTTAAATGAA
TGGACAACAATGTACAGTTTTTACTATGTGGCCACTGGTTTAAAGAGTGTGACTTTGTTTTCTCATTGAGTTTTGGG
AGGAAAAGGGACTGTGCATTGAGTTGGTTCTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAA
CTATAGTTAGTTGTGATTTGTGATTTTACTCTATTATTGTTTGTATGTTTTTCTCATTTCGTTTGTGGGTT
TTTTTTTCCAACGTGTATCTCGCTTGTCTTACAAGCAACCCAGGGTCCCTTCTTGGCACGTAAACATGTACGTATT
TCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTTATTATCATGTTATCTTATTAAAGAAAAAGCCCAAAAGC

FIGURE 24

MARFGLPALLCTLAVLSAALLAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQGST
CCSQEMEELKYSLSQKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAAKSLNDMFVKTYGH
LYMQNSELFKDLFVELKRYVVGNNLEEMLNDFWARLLERMFLVNSQYHFTDEYLECVSKYTE
QLKPFQDVPRKLLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRGL
VTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIESVMDPIDVKISDAIMN
MQDNSVQVSQKVFQCGGPPKPLPAGRISRSESASFARFRPHHPEERPTTAAGTSLDRLVTDVK
EKLKQAKKFWSSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLFAVTGNGLANQGNNEVQVDT
KPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAG
KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

Important features:

Signal peptide:

amino acids 1-22

ATP/GTP-binding site motif A (P-loop).

amino acids 515-524

N-glycosylation site.

amino acids 514-518

Glycosaminoglycan attachment sites.

amino acids 494-498, 498-502

N-myristoylation sites.

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

Glypicans proteins.

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

FIGURE 25

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC
CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACT
TACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAA
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCACAGGGACCGAGGC
CAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAAAGATTGGTTCCTGAG
AGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCCCTGTGATCATT
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATTCCAGA
GCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTG
AGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTC
TTCTTCTCCCACTCACTCTCCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCA
TGTTTTTCAAGATCATTTTGTGTTGCTCTCTCTAGTGTCTTCTCTCTCGTCAGTCTTAGCCT
GTGCCCTCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCT
AGCTAGTGTCAATTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTT
AAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 26

MKVLISLLLLLLPIMLSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFM
TVSGLPKKQCPDHFKNVKKTRHQRHHRKPNKHSRACQQLKQCQLRSFALPL

Important features:

Signal peptide:

amino acids 1-22

N-myristoylation sites.

amino acids 27-33, 46-52

FIGURE 27

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAG
AGCTGGTCTGCCATGGACATCCTGGTCCCCTCCTGCAGCTGCTGGTGCTGCTTCTTACCCTGCC
CCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCTGTGCAAAAGCTACTTCCCCTACCTGA
TGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAG
ATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGGCTGCGGAACCGGAGC
CAACTTTTCACTTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAAATCCCCACTTTGAGA
AGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGGCTCCT
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGCTGTG
CTCTGTGCAGAGCCCAAGGAAGTCTGTCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGC
TCTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTT
GAGCCCACCTGGAAACACATTGGGGATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGA
GAACGCCCAGTTCTCCGAAATCCAAATGGAACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTG
GGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCAAGCTCCAAGGCACTCATTTGCTCC
TTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTTA
GCAGAATGAGAGAAGACATTTCATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGG
AAACACTAGGACCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCAACGTTTGCCCTC
CCAATGTTGTCCCTTTCCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCCTCCTGAGGCTACAC
CCATGCGTCTCTAGGAACTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGAC
CCTCTCTCCCCACTACCACCTTCTTCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGG
ATGCCAGAGCAAGACTCAAAGAGGCAGAGTTTTGTCTCAAATATTTTTTAATAAATAGACGAA
ACCACG

FIGURE 28

MDILVPLLQLLVLLLTLP LHL MALLGCWQPLCKSYFPYLM AVLTPKSNRKMESKKRELFSQIKGL
TGASGKVALLELGCGTGANFQFYPPGCRVTC LDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM
RQLADGSMDVVVCTLVLC SVQSPRKVLQEVRRVLRPGGV LFFWEHVAEPYGSWAFMWQQVFPTW
KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWL PVGPHIMGKAVKQSFPSKALICSFPSL
QLEQATHQPIYLPLRGT

Important features:

Signal peptide:

amino acids 1-23

Leucine zipper pattern.

amino acids 10-32

N-myristoylation sites.

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

FIGURE 29

CAATGTTTGCCTATCCACCTCCCCCAAGCCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCTGCT
GCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCCAGAAAGTCTCTTCTG
CCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTCCTGCCTCAT
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGTGGGGGATGGCTA
AGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGGGCTGCCTTATTTAAA
GTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTTCATTAAGAAATT
GTTCCCTTCCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGTAAATATGTCTTTATAATAAAC
AGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 30

MLLLTLLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQPRG
EGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 31

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAGTT
CCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT
ATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAATCATGTCGG
GAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTGGCCATGATGTTTACC
TTCAGATTCATCACCACCTTCTGGTTCACATTTTCATTTTCATTGGTTATTTTGGGATTGTTGTT
TGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATAGAATTGGACA
CAGAAAGGGAAAAATGAAGTGCCTGCTGGGGTTTGCTATCGTATCCACAGGCATCACGGCAGTG
CTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAATCAC
AAATAAAGCCATCAGCAGTGCTCCCTTCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCA
TTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTGAGCCTGGGAAGTGCAGGAGCTGCCAGGTT
ATGGAAGGCGGCCAAGTGGAATATAAGCCCTTTCGGGCATTCCGTACATGTGGTGTACCATTT
AATTGGCCTCATCTGGACTAGTGAATTCATCCTTGCCTGCCAGCAAATGACTATAGCTGGGGCAG
TGTTTACTTGTTATTTCAACAGAAGTAAAAATGATCCTCCTGATCATCCCATCCTTTCTGCTCTC
TCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAG
GATTCCGAGAATCATTGTGATGTACATGAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT
CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTC
AACCAGAATGCATATACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAGATGC
ATTCAAATCTTGTTCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAA
TTTTTCTAGGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTAC
AATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGC
CCATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTTGATC
TGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTTCGTA
AAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGAATGAGGA
GGGAACAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATT
TCCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTT
TTAAAGACCTAATAAACCTATTCTTCTCTCAAAA

FIGURE 32

MSGRDTILGLCILALALSLAMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYDTNDLSIE
LDTERENMKCVLGFVAVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLFQPLWTFA
ILIFFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQOMTIA
GAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIIPRIIVMYMQNALKEQQHG
ALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD
FIIIFLGKVLVVCFTVFEGGLMAFNYNRAQVWAVPLLLVAFFAYLVVHSELSVFETVLDALFLCFA
VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSRNEEGTELQAIVR

Important features:

Signal peptide:

amino acids 1-20

Putative transmembrane domains:

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

N-glycosylation sites.

amino acids 204-208, 295-299, 313-317

N-myristoylation sites.

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

FIGURE 33

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGACCTCTCCCTGTTTCTTCCTTAGA
 ATAATTTGTATGGGATTTGTGATGCAGGAAAGCCTAAGGGAAAAAGAATATTCATTCTGTGTGGT
 GAAATTTTTTTGAAAAAAAATTCGCTTCTCAAACAAGGGTGTCAATCTGATATTTATGAGGAC
 TGTGTTCTCCTATGAAGGCATCTGTTATTGAAATGTTCTTGTGTTGCTGGTACTGGAGTAC
 ATTCAAACAAAGAAACGGCAAAGAAGATTAAGGCCCCAAGTTCACGTGTCCTCAGATCAACTGC
 GATGTCAAAGCCGGAAAGATCATCGATCCTGAGTTCATTGTGAAATGTCCAGCAGGATGCCAAGA
 CCCCAAATACCATGTTTATGGCACTGACGTGTATGCATCCTACTCCAGTGTGTGTGGCGCTGCCG
 TACACAGTGGTGTGCTTGATAATTCAGGAGGGAAAATACTTGTTCGGAAGGTTGCTGGACAGTCT
 GGTACAAAGGGAGTTATTCCAACGGTGTCCAATCGTTATCCCTACCACGATGGAGAGAATCCTT
 TATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTAACTACCCATCAGCTCTTACATACTCATCAT
 CGAAAAGTCCAGCTGCCCAAGCAGGTGAGACCACAAAAGCCTATCAGAGGCCACCTATTCCAGGG
 ACAACTGCACAGCCGGTCACTCTGATGCAGCTTCTGGCTGTCACTGTAGCTGTGGCCACCCAC
 CACCTTGCCAAGGCCATCCCCCTTCTGCTGCTTCTACCACCAGCATCCCAGACCACATCAGTGG
 GCCACAGGAGCCAGGAGATGGATCTCTGGTCCACTGCCACCTACACAAGCAGCCAAAACAGGCC
 AGAGCTGATCCAGGTATCCAAAGGCAAGATCCTTCAGGAGCTGCCTTCCAGAAACCTGTGGAGC
 GGATGTCAGCCTGGGACTTGTTCAAAAGAAGAATTGAGCACACAGTCTTGGAGCCAGTATCCC
 TGGGAGATCCAAATGCAAAATTGACTTGTCTGTTTTAATTGATGGGAGCACCAGCATTTGGCAA
 CGGCGATTCCGAATCCAGAAGCAGCTCCTGGCTGATGTTGCCCAAGCTCTTGACATTGGCCCTGC
 CGGTCCACTGATGGGTGTTGTCCAGTATGGAGACAACCTGCTACTCACTTTAACCTCAAGACAC
 ACAGGAATTTCTCGAGATCTGAAGACAGCCATAGAGAAAAATTACTCAGAGAGGAGGACTTCTAAT
 GTAGGTCGGGCCATCTCCTTTGTGACCAAGAACTTCTTTTCCAAAGCCATGGAACAGAAGCGG
 GGCTCCCAATGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
 GACTTGCGAGAGAGTCAGGAATCAACATTTTCTTCATCACCATTGAAGGTGCTGCTGAAAATGAG
 AAGCAGTATGTGGTGGAGCCCACTTTGCAAAACAAGGCCGTGTGCAGAACAAACGGCTTCTACTC
 GCTCCAGTGCAGAGCTGGTTTGGCCTCCACAAGACCCTGCAGCCTCTGGTGAAGCGGTCTGCG
 AACTGACCGCCTGGCCTGCAGCAAGACCTGCTTGAACCTGGCTGACATTGGCTTCGTATCGAC
 GGCTCCAGCAGTGTGGGGACGGGCAACTTCCGCACCGTCCAGTTTGTGACCAACCTCACCAA
 AGAGTTTGAGATTTCCGACACGGACACGGCATCGGGGCCGTGCAGTACACCTACGAACAGCGGC
 TGGAGTTTGGGTTCGACAAGTACAGCAGCAAGCCTGACATCCTCAACGCCATCAAGAGGGTGGGC
 TACTGGAGTGGTGGCACCAGCACGGGGCTGCCATCAACTTCGCCCTGGAGCAGCTCTTCAAGAA
 GTCCAAGCCCAACAAGAGGAAGTTAATGATCCTCATCACCAGCGGGAGGTCTTACGACGACGTCC
 GGATCCCAGCCATGGCTGCCATCTGAAGGGAGTGATCACCTATGCGATAGGCGTTGCCCTGGCT
 GCCCAGAGGAGCTAGAAGTCATTGCCACTCACCCGCCAGAGACCACTCCTTCTTTGTGGACGA
 GTTTGACAACCTCCATCAGTATGTCCCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCAC
 AGCCTCGGAAC**TGA**ATTAGAGCAGGCAGAGCACCAGCAAGTGCTGCTTTACTAACTGACGTGTT
 GGACCACCCACCGCTTAATGGGGCAGCACGGTGCATCAAGTCTTGGGCAGGGCATGGAGAAAC
 AAATGCTTGTATTATTCTTTGCCATCATGCTTTTTCATATTTCCAAAACCTGGAGTTACAAAGA
 TGATCACAAACGTATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACAT
 TTTGACAATTGTTTTCAAATAAATGTTTCGAATACAGTGCAGCCCTTACGACAGGCTTACGTAG
 AGCTTTTGTGAGATTTTAAAGTTGTTATTTCTGATTTGAACCTCTGTAACCTCAGCAAGTTTCAT
 TTTTGTGATGACAATGTAGGAATTGCTGAATTAATGTTTAGAAGGATGAAAAATAAAAAAAA
 AA
 AAG

FIGURE 34

MRTVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG
CQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWR
ESFIVLESKPKKGVTPSALTYSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVA
TPTTLPRPSPSAASTTIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQRQDPSGAAFQKP
VGADVSLGLVPKEELSTQSLEPVS LGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI
GPAGPLMGVVQYGDNPATFNLKHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN
RSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAVCRTNG
FYSLHVQSWFGLHKTQLQPLVKRVC DTRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTN
LTKEFEISD TDTRIGAVQYTYEQRL EFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALEQL
FKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAAQEELEVIATHPARHDSFF
VDEFDNLHQYVPRIIQNICTEFNSQPRN

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 181-200

N-glycosylation sites.

amino acids 390-394, 520-524

N-myristoylation sites.

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

Amidation site.

amino acids 304-308

FIGURE 35

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGC
CAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGTTTTAATTAAGCATGGAAT
ACAGAAAACAACAAAAAATAAGCTTTAATTTTCATCTGGAATCCACAGTTTCTTAGCTCCCTGGACCC
GGTTGACCTGTTGGCTCTTCCCCTGGCTGCTCTATCACGTGGTGTCTCCGACTACTCACCCCGAGTGTA
AAGAACCCTTCGGCTCGCGTGCTTCTGAGCTGCTGTGGAATGGCCTCGGCTCTCTGGACTGTCTTCCGAGTA
GGATGTCACTGAGATCCCTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTAC
CTCAGCCTTCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTTA
CAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAATGCTCTCATCAAAATCCATTTCTGGTCATTTC
TGGTGACCTCCCACCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCT
TGTTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAATGTTGGC
ATTGTCTTAGAGGATGAACACCTTCTTTATGGTGACATAATCCGACAAGATTTTTTAGACACATATAATA
ACCTGACCTTGAAAACCATTTATGGCATTGAGGTGGGTAAGTGAAGTTTGGCCCAATGCCAAGTACGTAATG
AAGACAGACACTGATGTTTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGA
GAAGTTTTTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCATATTT
CTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTATATATAATGTCCAGAGAT
TTGGTGCCCAAGGATCTATGAAATGATGGGTACGTAACCAATCAAGTTTGAAGATGTTTATGTCCGGGAT
CTGTTTGAATTTATTAAGTGAACATTCAATTCAGAAGACACAAATCTTTCTTCTATATAGAATCC
ATTTGGATGTCTGTCACTGAGACGTGTGATTGCAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTT
TGGCAGGTGCTGCTAAGGAACACCACATGCCATTATTAAGTTCACATTCTACAAAAAGCCTAGAAGGACAG
GATACCTTGTGAAAGTGTTAAATAAGTAGGTACTGTGGAATTCATGGGGAGGTCAGTGTGCTGGCTT
ACACTGAACTGAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTCAGG
CCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGG
ACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGGTGTACTGAGTTATAAGCTCA
CTAGGCTGTAAAAACAAAACATGTAGAGTTTATTTATTGAACAATGTAGTCACTGAAGGTTTTGTGTA
TATCTTATGTGGATTACCAATTTAAAAATATATGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATA
CTGAACAAAATTTTACCTGTTTTTGGTCATTATATAAGTACTTCAAGATGTTGCAGTATTTACAGTTATT
ATTATTTAAATTAATCACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAG
TGAATCATTCTTTACATGCAACATTTCCAGTACTTAACTGATCAGTTTATTATTGATACATCACTCCA
TTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGACTTTGTAAATATTTTACTGTGGT
AATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

FIGURE 36

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQDFHF
TLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EKEDKMLA
LSLEDEHLLYGDIIRQDFLDTYNNLT LKTIMAFRWVTEFCPNAKYVMKTD TDVFINTGNLVKYL
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQYEPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHV
KPIKFEDVYVGICLNLKVNIIHIPEDTNLFFLYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR
NTTCHY

Important features:

Type II transmembrane domain:

amino acids 20-39

N-glycosylation sites.

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

Glycosaminoglycan attachment site.

amino acids 239-243

Ly-6 / u-PAR domain proteins.

amino acids 23-37

N-myristoylation site.

amino acids 271-277

FIGURE 37

CGCTCGGGCACCAGCCGCGGCAAGGATGGAGCTGGGTTGCTGGACGCAGTTGGGGCTCACTTTTCTTCAGCTCCTTCTCATC
TCGTCCTTGCCAAGAGAGTACACAGTCATTAATGAAGCCTGCCCCGAGCAGAGTGAATATCATGTGTCGGGAGTGTGTG
AATATGATCAGATTGAGTGCCTGCCCCGGAAGAGGGAAGTCGTGGGTTATACCATCCCTTGTGTCAGGAATGAGGAGAA
TGAGTGTGACTCCTGCGTATCCACCCAGGTTGTACCATCTTTGAAAACGCAAGAGCTGCCGAAATGGCTCATGGGGGGT
ACCTTGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTG
GCCAGGTTCTGCGAGCCCCAAAGGGTCAGATTTTGTGGAAAGCTATCCCTAAATGCTCACTGTGAATGGACCATTCATGC
TAAACCTGGGTTTGTATCCAACTAAGATTGTTCATGTTGAGTCTGGAGTTGACTACATGTGCCAGTATGACTATGTTGAG
GTTTCGTGATGGAGACAACCGCATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAG
GATCCTCACTCCACGTCCTCTTCCACTCCGATGGCTCCAAGAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGC
ATGCTCCTCATCCCTTGTTCATGACGGCAGTGCCTCTTGACAAGGCTGGATCTTACAAGTGTGCCTGCTTGGCAGGC
TATACTGGGCGAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCCCTGGGGGCCAGTCAATGGGTACAGAAAA
TAACAGGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAAATGGCACCGTGGTGTCTTCTTTTGAACACTCCTATGT
TCTTAGTGGCAATGAGAAAAAGAACTTGCCAGCAGAAATGGAGAGTGGTCAAGGAAACAGCCATCTGCATAAAAGCCTGCCGA
GAACCAAGATTTTCAGACCTGGTGAGAAGGAGAGTTCCTCCGATGCAGGTTCAAGGAGACACCATTACACAGCTAT
ACTCAGCGGCTTTCAGCAAGCAGAACTGCAGAGTGGCCCTACCAAGAAGCCAGCCCTTCCCTTGGAGATCTGCCCATGGG
ATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACCTTCTACCGCCGCTGGGCGAGCAGAGGAGCATGT
CTGAGGACTGGGAAGTGGAGTGGGCGGGCACCATCTGCATCCCTATCTGCGGGAAATGAGAACATCACTGCTCCAAAGA
CCCAAGGGTTGCGCTGGCCGTGGCAGGCAGCCATCTACAGGAGGACAGCGGGGTGCATGACGGCAGCCTACACAAGGGAGC
GTGGTTCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCACTGTGTTACTGACCTGGGGAG
GTCACCATGATCAAGACAGCAGACCTGAAAGTTGTTTTGGGGAAATTTACCGGGATGATGACCGGGATGAGAAGACCATCC
AGAGCCTACAGATTTCTGCTATCATTCTGCATCCCAACTATGACCCCATCCTGCTTGATGCTGACATCGCCATCTGAAGCT
CCTAGACAAGGCCCGTATCAGCACCCGAGTCCAGCCCATCTGCCTCGCTGCCAGTGGGATCTCAGCACTTCCCTCCAGGAG
TCCCACATCACTGTGCTGGCTGGAATGTCTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACATGCGCTCTGGGG
TGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGAGTGTCACTGATAACATGTT
CTGTGCCAGCTGGGAACCCACTGCCCTTCTGATATCTGCATGACAGACAGGAGGCATCGCGGCTGTGCTTCCCGGGA
CGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCA
CTGCCCTTACCAAGGTGCTGCCCTTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAG
TGTTTCTGTATATCCGTCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGCCTGAAGTGTGATTGGCCTGTGAAGTGGCT
GTGCCAGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAGTAGACCTCCATTGCTGGTAGGCTGATGCCGCTCCA
CTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAAGAAGTAAGTTTCTTCAAGAAGACCATATACAAAACCTCTCCA
CTCCACTGACCTGGTGGTCTTCCCAACTTTTCAGTTATACGAATGCCATCAGCTTGACCAGGGAAGATCTGGGCTTCATGAG
GCCCCTTTTGAGGCTCTCAAGTTCTAGAGAGCTGCCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCCCTT
TGTGTACATGGCCACAGTACAGTCTGGTCTTTTCTTCCCATCTCTTGTACACATTTTAATAAAATAAGGGTTGGCTTCT
GAACTACAAAAA
AA
AA

FIGURE 38

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYT
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGDCMRGQ
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDQII
KRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC
ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNNSYVLSGNE
KRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPLHQLYSAAFSKQKLQSAPTK
KPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP
KTQGLRWQPQAIIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADL
KVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR
DLSTSFAQESHITVAGWNVLADVRSPGFKNDTLRSGVSVVDSLLCEEQHEDHGIPVSVTDMFCA
SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMLVSWSYDKTCSHRLSTAFTKVLPFKDWI
ERNMK

Important features of the protein:

Signal peptide:

amino acids 1-23

EGF-like domain cysteine pattern signature.

amino acids 260-272

N-glycosylation sites.

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

N-myristoylation sites.

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,
474-480, 491-497, 638-644, 666-672

Amidation site.

amino acids 56-60

Serine proteases, trypsin family.

amino acids 489-506

CUB domain proteins profile.

amino acids 150-167

FIGURE 39

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCGTGATTTATTAACGTGGCTTAATC
TGAAGGTTCTCAGTCAAATCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGCTTGGCTGG
TTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGGCGCTTCTGTTGC
TGGTCTTGCCCTGGCTCAGTCCCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCTGTATTCAGAACTCTGTA
AAGTGCCCTCCACTACGGCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAGACGGCTGTGCGAGCC
TCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAATGACAGACGAGCCTGGCCTAGACA
ACCTTGCTTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCAGTGGACTCTGGCCGGAGCAACCGAATA
GGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAAATCGAGCTTTGAGTGTTCTTCGAA
GGACAAGAGCGGGAGTGCAAGTGGCAACCATGCCGACAGGGCAGGGAAAATTCTGAAAACACCACTGCCCTGAAG
TCTTTCGAAGGTTGTACCACCTGATTCCAGATGGTGAAATTACCAGCATCAAGATCAATCGAGTAGATCCAGTGAAA
GCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCCATATCATTATCCAACACATTATCGTGATGGGG
TGATGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTC
ACAACTAGCTGTGCGTCTCCTGCGGCAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCCA
GCAGGAACATGGACAGGCCCCGATGCCTACAGACCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCC
CCGAGGAGCAGCTTGAATAAACTGGTGCGCAAGGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCG
GTGTGGCATATCGACATGGTCAGCTTGAGGAGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCA
GCCCCAGAAAGTGGGCTCATCTGATTGAGGCCAGTGAAAGACGTGTTACCTCGTGTGTCGCCAGGTTCCGGCAGC
GGAGCCCTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCAGGGCCAGGGGAGAGGCAACA
CTCCCAAGCCCTCCATCTACATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAGACCCCGGTGAATCTCTCG
GCATGACCGTCGAGGGGAGCATCACATAGAGAATGGGATTGCTATCTATGTCATCAGTGTGAGCCCGAGGAG
TCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTTTGTGAATGTGGATGGGTCGAACTGACAGAGGTCAGCC
GGAGTGAGGCAGTGGCATTATTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTGGAAAGTCAAAGAGTATGAGC
CCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCCATCCT
GGGTGATGTGGCTGGAATTACCACGGTGCTTGTATACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAATC
TGGGCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAAACAAACCTTTTTTCATCAATCCATTGTTGAAGGAA
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTGCTGTCAATGGTAGAAGTACATCAGGAATGA
TACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTCTTGGCCTGGCACTT
TTTTTATGAATCAATGATGGGTGAGGAGGAAACAGAAAATCACAATAGGCTAAGAAGTTGAAACACTATATTTATC
TTGTGAGTTTTTATATTTAAAGAAAGATACATTGTAAAAATGTCAGGAAAAGTATGATCATCTAATGAAAGCCAGTT
ACACCTCAGAAAATATGATTCAAAAAATTAAGTACTAGTTTTTTTTTCAAGTGTGGAGGATTTCTCATTACTCTAC
AACATTGTTTATATTTTTCTATTCAATAAAAGCCCTAAACAACTAAATGATTGATTGTATACCCCACTGAATT
CAAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGGTACATTATGGCCATTTTAAATTTACAGCT
AAAATATTTTTTAAATGCATTGCTGAGAAACGTTGCTTTCATCAACAGAATAAATATTTTTTCAGAAAGTTAAA

FIGURE 40

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPS
PEVSAAATISLMTDEPLDNPAYVSSAEDGQPAISPVDSESRNSNRTRARPFFERSTIRSRSFKKINR
ALSVLRRTKSGSAVANHADQGRESENTTAEVFPRLYHLIPDGEITSIKINRVPSESLSIRLV
GGSETPLVHIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVM
REQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGVFIENVLDGGVAYRHG
QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRSPDIFQEAGWNSNGSWSPG
PGRSNTPKPLHPTITCHEKVNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVISRDGR
IKTGDILLNVGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPP
SDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDG
RIRCGDILLAVNGRSTSGMIHACLARLLKELKGRITLTIVSWPGTFL

Important features:

Signal peptide:

amino acids 1-15

N-glycosylation sites.

amino acids 108-112, 157-161, 289-293, 384-388

Tyrosine kinase phosphorylation sites.

amino acids 433-441, 492-500

N-myristoylation sites.

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,
467-473, 603-609

FIGURE 41

ACCAGGCATTGTATCTTCAGTTGTTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT
CTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGCTTCAACCTGACT
TTCCACCTTTCCCTACAAATCCGATTACTGTTGCTGTTGACTTTGTGCCTGACAGTGGTTGGGTGGGC
CACCAGTAACTACTTCGTGGGTGCCATTCAAGAGATTCTTAAAGCAAAGGAGTTCATGGCTAATTTCC
ATAAGACCCCTCATTTTGGGGAAGGGAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAATT
GACAACTGTCTTCTGTGTCTCCTTACCTCAGAGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCAC
TTTGGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAG
CTTTACAGAGGGTGCCTCCTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAA
CATCTGCATCCCTTCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTATCCACCAGGCTGAAGG
TAAAAAGTTTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGG
ACTGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAG
CATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTGG
GGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTCAGGTGAATGGATTCTCTAACAACTACTGGGGAT
GGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGGCCCTG
CCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG
GATGAAGCTCTTACACCAAGTGTACGAGTCTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAAT
TAGTATCTGTGGAACACAATCCTTTATATATCAACATCACAGTGGATTCTGGTTTGGTGCATCAGCC
TGATCTTTTGGTGATGTTTGGGAAGAACTGATTCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAA
ATAGTAGCACACATTAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTCTTTTGTATTTTCT
TAGCAGAGCTCCTGGTGATGTAGAGTATAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGAT
CATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGATAA
AATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTATTTAAATTTGAAGTAATATATTATGGGAT
AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAA
AGGTACGAAGATACAATACTGTTATTTCATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTGAGGT
GAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAAGTTGGGAATGAAGA
GGTAGCAGGAGGGTGGAGTGTGCGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC
CTTCAGGGGAGGACCTGCCAGGTATGCCTTCCAGTGTGCCCACCAGAGAATACATTCTCTATTAGT
TTTTAAAGAGTTTTTGTAAATGATTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACAT
ATTAACATAATAAATATGTCTATCAAATACCTCTGTAGTAAATGTGAAAAGCAAAA

FIGURE 42

MGENLTFHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTILGKGKTLTN
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPH
RNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKGKFNRAKLLNVGYLEALKEENWDCFIHFDV
DLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGQVTALSREQFFKVNGFSNNYWGWGGED
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRTDGLSSCSYKLV
SVEHNPLYINITVDFWFGA

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 4-8, 220-224, 335-339

Xylose isomerase proteins.

amino acids 191-202

FIGURE 43

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCTGGG
CCGCTTGCCTCCTGCTCCTCCTCCTCCTCGCCAGCCTGACCACTGGCTCTGTTTTCCCACAACAG
ACGGGACAACCTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCCAT
GTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCTGCGGCTGCTGTC
ATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTGCCCCGTCCCCTCCC
TTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGAATAAAATGGCTGGTTCTTTTGT
TCCAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 44

MALSSQIWAACLLLLLLSLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPI
CIFCCGCCHRSKCGMCCKT

Important features:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 58-59

N-myristoylation site.

amino acids 44-50

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 1-12

FIGURE 45

GTGGCTTCATTTAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCC
TCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT
TCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTG
GACCTTCAACACAACCCCTCTGTCCACATACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAAGTGAAG
AAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCA
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATT
TATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTC
CTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCCTGTCAGCAGAACT
TCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCCATG
GTCCTCCTGTGTCTCCTGTTGGTGGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTCTTTG
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGACATTTGTCTGGG
AACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT
AGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT
GGAAATCCCCACTCACTGCTCAGGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTA
TCTAGACAGCAGTGCACTCCCCTAAGTCTCTGCTCA

FIGURE 46

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQP
EGGTIIIVTQNRNRERVDFFDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK
PKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFIC
VARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFLGLFLWFLKRERQEEYIE
EKKRVDICRETPNICPHSGENTEYDTIPHTNRITLKEDPANTVYSTVEIPKKMENPHSLLTMPDT
PRLFAYENVI

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 224-250

Leucine zipper pattern.

amino acids 229-251

N-glycosylation sites.

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,
291-295

FIGURE 47

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCCGAAGGATGGACATCCTGCAATGG
ATTGAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCCGATACCTCTAATTGTCAGCT
TAGTTGAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGTTCCCAGGAATT
ATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG
CTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCACAGTCATTGGTGCTC
TGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCTCTCATGTGTAATTCTCCAAGC
AACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTCATCCAGAATCCTTCAA
CTTGCAAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTTCAATAAACCCACCAGTAACG
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGG
CTTATCCACTTCTCAGTATTTTTAGGTCTATTGCTTGTGGAATTCCTGGAGGTCCTGTTGGGCT
CAGTCAGATAGTCATCGGTTTCTTGGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTG
TGTAGTTTAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAAAAAA

FIGURE 48

MTCCEGWTS CNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA
TTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNSPNSNANCEFSL
KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIHFSVFLGL
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

Important features:

Transmembrane domains:

amino acids 10-31 (type II), 50-72, 87-110, 191-213

N-glycosylation sites.

amino acids 80-84, 132-136, 148-152, 163-167

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 223-227

N-myristoylation sites.

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 207-218

TNFR/NGFR family cysteine-rich region protein.

amino acids 4-12

FIGURE 49

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGA
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG
ATCCGTGGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCCTCGAACTGTGA
CATGGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGAAGCCAATGACC
CATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC
TGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAAATGCAAATACAAGAG
CAGCCAGAAGCAGCACAGTCCCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTCTGCCA
CTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACC
TCCTCCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCT
TTCTGATCAGGAGGCTTCTTTATGAATTAAACTCGCCCCACCACCCCTCA

FIGURE 50

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKS
SQKQHSPVPEKAIP LITPGSATTC

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 36-59

N-myristoylation sites.

amino acids 41-47, 45-51, 84-90

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.

amino acids 54-67

FIGURE 51

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG
AGGACAGGGAGTCCGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCGGCAAGG
AGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATGAAGTTCCAG
GGGCCCCCTGGCCTGCTCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGGCCCCCTGCAGAG
CGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCCTGGGAGACGCCCTGA
GCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGGAGGGGCAGCTGGCTCTAAAGTCAGTGAG
GCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAGGCAGGTTCCAGGCTTTGGCGC
AGCAGATGCTTTGGGCAACAGGTCGGGGAAGCAGCCCATGCTCTGGGAAACACTGGGCACGAGA
TTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCAGATGCTGTCCCGGCTCCTGGCAGGGG
GTGCTTGGCCACAGTGGTGTCTGGGAAACTTCTGGAGGCCATGGCATCTTTGGCTCTCAAGGTGG
CCTTGGAGGCCAGGGCCAGGGCAATCCTGGAGGTCTGGGGACTCCGTGGGTCCACGGATAACCCCG
GAAACTCAGCAGGCAGCTTTGGAATGAATCCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGA
GGGCCACCAAACCTTTGGGACCAACACTCAGGGAGCTGTGGCCCAGCCTGGCTATGGTTCAGTGAG
AGCCAGCAACCAGAATGAAGGTGCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA
ACTCTGGGGGAGGCAGCGGCTCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAAC
AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAG
TGGCGGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGT
CCTCCTGGGGATCCAGCACCGGCTCCTCCTCCGCAACCACGGTGGGAGCGGCGGAGGAAATGGA
CATAAACCCGGGTGTGAAAAGCCAGGGAATGAAGCCCGGGAGCGGGGAATCTGGGATTCAGGG
CTTCAGAGGACAGGGAGTTTCCAGCAACATGAGGGAATAAGCAAAGAGGGCAATCGCCTCCTTG
GAGGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGTT
GGTGGAGTCAATACTGTGAACCTCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCTGGAA
GAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGAAGCTCTC
GCATCCCCGTGACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCCACTCCCTCCTTAA
AACACCACCTCTCATCACTAATCTCAGCCCTTGCCTTGAATAAACCTTAGCTGCCCCACAAA
AA
AA

FIGURE 52

MKFQGPPLACLLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIKKEAGGAAGSKVS
EALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGADAVRGSWQGVF
GHSGAWETSGGHGIFGSQGGGLGGQGGNPGGLGTPWVHGYPGNSAGSFGMNPQGAPWGQGGNGGPPNF
GTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGSGSQSGSSGSGSNGDNNNGSSSGGS
SSGSSSGSSSGSGSGSGSGSGNSGGSRGDSGSESSWGSSSTGSSSGNHGGSGGGNGHKPGCEKPGNE
ARGSGESGIQGRGQVSSNMREISKEGNRLLGGSGDNYRGQSSSWGSGGGDAVGGVNTVNSETPGM
FNFDTFWKNFKSKLGFINWDAINKDQRSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80,
90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161,
159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224,
236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252,
253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285,
283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301,
298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329,
325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,
387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 53

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG
CTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCT
ACTGCGCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACGCGCCGGCTCCAGTGTTTCC
CACAGCCCCAAAACGGAACGTGTTTTGGGGTCACCTGGGCCTGATCACTCCTACAGAGGAGGGC
TTGAAGGACTCGACCCAGATGTGCGCCACCTATTCCCAGGGCTTTACGGTATGGCTGGGTCCCAT
CATCCCCCTTCATCGTTTTATGCCACCTGACACCATCCGGTCTATACCAATGCCTCAGCTGCCA
TTGCACCCAAGGATAATCTCTTCATCAGGTTCCCTGAAGCCCTGGCTGGGAGAAGGGATACTGCTG
AGTGGCGGTGACAAGTGGAGCGGCCACCGTCGGATGCTGACGCCCGCCTTCCATTTCAACATCCT
GAAGTCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGG
CCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGGACAGTCTA
CAGAAATGCATCTTCAGCTTTGACAGCCATTGTGAGGAGAGGCCAGTGAATATATTGCCACCAT
CTTGAGCTCAGTGCCCTTGTAAGAAAAGAAGCCAGCATATCCTCCAGCACATGGACTTTCTGT
ATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGAC
GCTGTCATCCGGGAGCGCGTCGCACCTCCCACTCAGGGTATTGATGATTTTTTCAAAGACAA
AGCCAAGTCCAAGACTTTGGATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG
CATGTGTCAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGAGAGCCATGACACCAG
GCCAGTGGCCTCTCCTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCG
ACAGGAGGTGCAAGAGCTTCTGAAGGACCGCATCCTAAAGAGATTGAATGGGACGACCTGGCCC
AGCTGCCCTTCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATC
TCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTG
CCTCATCGATATTATAGGGGTCCATCACAACCAACTGTGTGGCCGGATCCTGAGGTCTACGACC
CCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCTTTCTCCGCA
GGGCCCAGGAAGTGCATCGGGCAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCTGGCGTTGAT
GCTGCTGCACTTCCGTTCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAATTGATCATGC
GCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCGAATGTAGGCTTGCACTGACTTTCTGAC
CCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGCTGTCAA

FIGURE 54

MSLLSLPWLGLRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRLQCFPPKRNWFWGHLG
LITPTEEGLKDSTQMSATYSQGFTVWLGPPIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP
WLGEGILLSGGDKWSRHRRLTPAFHFNIILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI
SLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC
RLVHDFTDAVIRERRRTLPTQGIDDFKDKAKSKTLDFIDVLLLSKDEDGKALSDEDIRAEADTF
MFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENSKGRSP
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN
VGLQ

Important features:

Transmembrane domains:

amino acids 13-32 (type II), 77-102

Cytochrome P450 cysteine heme-iron ligand signature.

amino acids 461-471

N-glycosylation sites.

amino acids 112-116, 168-172

FIGURE 55

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTTGA
GCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTTCTGCCT
TTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCATTGACGTGG
TACAGCCTTTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTTCCTGCGTGTGCTTGC
ATAATTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAGCTGGTGGACAGTTTT
GTAACATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCTTGCAGCAATGTGTTGCTT
GTGATTTCGAACATTTGAGGGTTACTTTTGAAGCAACAATACATTCTCGAACCTGAATGTCAGTA
GCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGGAATCTTCCTCATGTACCTGTTTCCTC
TCTGGATGTTGTCCCACTGAATCCCATGAATACAAACCTATTTCAGCAACAGCAAAAAAAAAAAAA
AA

FIGURE 56

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGALIFCILQSLALTWYSLSFIPFAR
DAVKKCFVCLA

Important features:

Signal peptide:

amino acids 1-33

Type II fibronectin collagen-binding domain protein.

amino acids 30-72

FIGURE 57

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCGAGTGGAGCACCCAGCAGGCGGCCAACATGCTCTGTCTGTGCCTG
TACGTGCCGGTTCATCGGGGAAGCCAGACCGAGTTCCAGTACTTTGAGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCC
ATTTTCAAGCTCAGTGTCTTCATCCCTCCAGGAATTTCCACCTACCGCCAGTGGAGCAGAAAAATTGTACAAGCT
GGAGATAAGGACCTTGATGGGCAGCTAGACTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGAGG
CTGGTGTTTAAGATTTTGGACAAAAAAGATGATGGACGCATTGACCGCAGGAGATCATGCAGTCCCTGCCGGACTTG
GGAGTCAAGATATCTGAACAGCAGGCGAGAAAAATTTCTCAAGAGCATGGATAAAACGGCAGCATGACCATCGACTGG
AACGAGTGGAGAGACTACCACCTCCTCCACCCGCTGGAAAACATCCCGAGATCATCCTCTACTGGAAGCATTCCACG
ATCTTTGATGTGGGTGAGAATCTAACGGTCCCGGATGAGTTACAGTGGAGGAGAGGCAGACGGGGATGTGGTGGAGA
CACCTGGTGGCAGGAGGTGGGGCAGGGGCCGTATCCAGAACCTGCACGGCCCCCTGGACAGGCTCAAGGTGCTCATG
CAGGTCCATGCCTCCCGCAGCAACAATGCGCATCGTTGGTGGCTTCACTCAGATGATTCCAGAAGGAGGGGGCCAGG
TCACTCTGGCGGGCAATGGCATCAACGTCTCAAAATTTGCCCGGAATCAGCCATCAAATTCATGGCCTATGAGCAG
ATCAAGCGCCTTGTGGTAGTGACAGGAGACTCTGAGGATTACGAGAGGGCTTGTGGCAGGGTCTTGGCAGGGGCC
ATCGCCAGAGCAGCATCTACCCATGGAGGTCTGAAGACCCGGATGGCGTGGCGAAGACAGGCCAGTACTCAGGA
ATGCTCGAGTGCAGCAGGAGGATCTGGCCAGAGAGGGGTGGCCGCTTCTACAAAGGCTATGTCCCAACATGTG
GGCATCATCCCTATGCCGGCATCGACCTTGCACTACGAGACGCTCAAGAATGCCTGGCTGCAGCATTATGCAGTG
AACAGCGCGGACCCCGGCTGTTTGTCTCCTGGCCTGTGGCACCATGTCCAGTACCTGTGGCCAGCTGGCCAGCTAC
CCCCTGGCCTAGTCAGGACCCGGATGCAGGCGCAAGCCTCTATTGAGGGCCTCCGGAGGTGACCATGAGCAGCCTC
TTCAAAACATATCTGCCGACCGAGGGGGCTTCGGGCTGTACAGGGGGCTGGCCCCAACTTCATGAAGTTCATCCCA
GGTGTGAGCATCAGCTAGTGGTCTACGAGAACCTGAAGATCACCTGGCGTGCAGTGCAGGTCGAGGGGAGGGG
CGCCCCGAGTGGACTCGCTGATCCTGGGCGCAGCCTGGGGTGTGCAGCCATCTCATTCTGTGAATGTGCCAACAT
AAGCTGTCTCGAGCCAAGCTGTGAAAACCTAGACGCACCCGAGGGAGGGTGGGGAGAGCTGGCAGGCCCCAGGGCTT
GTCCTGCTGACCCAGCAGACCCTCCTGTTGGTCCAGCGAAGACCACAGGCATTCTTAGGGTCCAGGGTCAAGCAGG
CTCCGGGCTCACATGTGTAAAGACAGGACATTTCTGCAGTGCCTGCCAATAGTAGCTTGGAGCCTGGAGGCCGGCT
TAGTTCCTTCCATTTACCCCTTGACGCCAGCTGTTGGCCAGGGCCCTGCCCTCTGGTCTGCCGTGCATCTCCTGTGC
CCTCTTGTGCTGCCCTGTCTGCTGAGGTAAGGTGGGAGGAGGGCTACAGCCACATCCCACCCCTCGTCCAATCCC
ATAATCCATGATGAAAGGTGAGGTACGTGGCCTCCAGGCCTGACTTCCCAACCTACAGCATTGACGCCAACTTGGC
TGTGAAGGAAGAGGAAAGGATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATG
CTTGGGAGTGCAGGGGGCTCGGGCTGCCTGGCCTGGCTGCACAGAAGGCAAGTGTGGGGCTCATGGTGTCTGAGCT
GGCCTGGACCTGTGAGATGGGCCCCACCTCAGAACCAACTCACTGTCCCACTGTGGCATGAGGGCAGTGGAGCA
CCATGTTTGAAGGCGAAGGGCAGAGCGTTTGTGTCTTGGGGAGGGAAGGAAAGGTGTTGGAGGCCTTAATTATGG
ACTGTTGGGAAAGGGTTTTGTCCAGAAGGACAAGCCGGACAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG
GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGGTCTCTGTCCAACCCAGCAGGGGGCGCAGC
GGGACCAGCCCCACATTCACCTTGTGTCACTGCTTGGAACTATTATTTTGTATTATTGAACAGAGTTATGTCTT
AACTATTTTATAGATTTGTTAATTAATAGCTTGTATTTCAAGTTCATTTTATTATTCATATTTATGTTTATGTT
GATTGTACCTTCCCAAGCCCGCCAGTGGGATGGGAGGAGGAGAGAAGGGGGGCTTGGGGCGCTGCAGTCACATCT
GTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAAGCGGCCAGAAAGGCAGCAGCCTGGCTCCTTTCTTTTGGCAG
GTTGGGGAAGGGCTTCCCCCAGCCTTAGGATTTAGGGTTTGAAGTGGGGCGTGGAGAGAGGGGAGAACCTCAAT
AACCTTGAAGGTGGAATCCAGTTATTTCTGCGCTGCGAGGGTTTCTTTATTTCACTCTTTTCTGAATGTCAAGGCAG
TGAGGTGCTCTCACTGTGAATTTGTGGTGGGCGGGGGCTGGAGGAGAGGGTGGGGGCTGGCTCCGTCCTCCCAGC
CTTCTGCTGCCCTTGTCTTAACAATGCCGGCAACTGGCGACCTCACGGTGTCACTTCCATTCACCAGAATGACCTGA
TGAGGAAATCTTCAATAGGATGCAAGATCAATGCAAAAATTTGTATATATGAACATATAACTGGAGTCGTCAAAAAG
CAAATTAAGAAAGAATTGGACGTTAGAAGTTGTATTTAAAGCAGCCTTCTAATAAAGTTGTTTCAAAGCTGAAAAA
AA

FIGURE 58

MLCLCLYVPVIGEAFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKDLDG
QLDFEETFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILKSMDKNG
TMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMWWRHLVAGGG
AGAVSRTCTAPLDRLKVLVQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIK
FMAYEQIKRLVGSQDETLEIRLHVAGSLAGAIQSSIYPMEVLKTRMALRKTGQYSGMLDCARR
ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNSADPGVFVLLACGTMSSTC
GQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV
VYENLKITLGVQSR

Important features:

Signal peptide:

amino acids 1-16

Putative transmembrane domains:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation sites.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 59

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGC
TTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG
CACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTGCGCTCAGCT
GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTTGAACCTGACATCAAACTTTCTGATAT
CGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAAAGATG
AGCTGTCTGGAGCAGGATGAAATGTTTTCAGAGGCCGGACAGCAGTGTTCGCTGATCAAGTGATAGTT
GGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT
CATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGG
AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCCTGTGAGGCTCCCCGATGGTTCCCC
CAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACCTTCTCGGAAGTCTCCAATAC
CAGCTTTGAGCTGAACTCTGAGAATGTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGA
TCAACAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTG
ACAGAATCGGAGATCAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGT
CTCTTCTTTCTTTGCCATCAGCTGGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAAATAAT
GTGCCTTGGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTTAC
CACCAGATATGACCTAGTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG
AGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAAGCAGAAGGCTCCAATATGAACAAGATAAAT
CTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTAGACAAGTGTGTTAAGA
GTGATAAGTAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT
CACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGC
TGTAATGTTGCTCTGAGGAAGCCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATCCAC
AAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCG
GCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTC
TCTTCCCACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTAGCATAAACAGAGCAGT
CGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 6o

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS
DIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKNVQLTDAGTYKC
YIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVS
NTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTSEIKRRSHLQLLNSKASL
CVSSFFAISWALLPLSPYMLLK

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 258-281

N-glycosylation sites.

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,
220-224

N-myristoylation sites.

amino acids 52-58, 126-132, 188-194

FIGURE 61

TGACGTCAGAATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAG
CACCAGGAGCCCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGT
GGGCTACCCCCTGGTGGTGGTTATGGGGGTCTGCCCTGGAGGGCCTTATGGACCACCAGCTGG
TGGAGGGCCCTATGGACACCCCAATCCTGGGATGTTCCCTCTGGAACCTCAGGAGGACCATATG
GCGGTGCAGCTCCCGGGGGCCCTATGGTCAGCCACCTCCAAGTTCTACGGTGCCAGCAGCCT
GGGCTTTATGGACAGGGTGGCGCCCCTCCCAATGTGGATCCTGAGGCCTACTCCTGGTTCCAGTC
GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA
ATTGGTCTTCATTCAATGATGAGACCTGCCCTCATGATGATAAACATGTTTGACAAGACCAAGTCA
GGCCGCATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGGAAGAACCTCTT
CCAGCAGTATGACCGGGACCCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCC
AAATGGGCTACAACCTGAGCCCCAGTTACCCAGCTTCTGGTCTCCCGCTACTGCCACGCTCT
GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGACCCAGCTGCAGGTGCTGACAGA
GGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGCTTCGAGGACTTCGTCA
CCATGACAGCTTCTCGGATGCTATGACCCCAACCATCTGTGGAGAGTGGAGTGCACCAGGGACCTT
TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTTCCTGTCCCTCTAGAAGAAC
ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTGCATCATAGCCACCA
AATAGTGAGGACCGGGGCTGAGGCCACACAGATAGGGGCCTGATGGAGGAGAGGATAGAAGTTGA
ATGTCCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCTTGTAATGG
AGTTAGTGTCAGTCAGCTGAGCTCCACCCTGATGCCAGTGGTGAGTGTTCATCGGCCTGTTACC
GTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAACGAGCCATTTTCTCCAAAGTGGAAT
CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGGATTCTGCCACACCATAAAT
CCTTGTTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT
CTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCTGCCATGCTCTGCTCGGCT
TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTAATTGCAATTTTTTTC
ATTTGGGGCCAAAAGTCCAGTGAATTTGTAAGCTTCAATAAAAGGATGAAACTCTGA

FIGURE 62

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG
HPNPGMFPSGTPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDS DH
SGYISMKELKQALVNCNWSSFNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDR
DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYPERSANPAMQLDRFIQVCTQLQVLTEAFREK
DTAVQGNIRLSFEDEFVTMTASRML

Important features of the protein:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 147-150

Casein kinase II phosphorylation sites.

amino acids 135-138, 150-153, 202-205, 271-274

N-myristoylation sites.

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-
66, 70-75, 78-83, 83-88, 87-92, 110-115

FIGURE 63

CAGGATGCAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCATC
TCCCAGGCCCTCTTTGCCCCGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCCAAACTTCGGGACC
AACTTGCCTCAGCTCGGACAACCTTCCTCCACTGGCCCCCTCTAACTCTGAACATCCGCAGCCCCG
TCTGGACCCCTAGGTCTAATGACTTGGCAAGGGTTCCTCTGAAGCTCAGCGTGCCTCCATCAGATG
GCTTCCCACCTGCAGGAGGTTCTGCAGTGCAGAGGTGGCCTCCATCGTGGGGGCTGCCTGCCATG
GATTCCTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGAGGACCGCCTGGGGGA
AGCGCTGCCTGAAGAACTCTTTACCTCTCCAGTGTGCGGCCCTCGCTCCGGGCAGTGGCCCTT
TGCTGGGGAGTCTTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGAC
TCGGAGTCCAGACGACTGCCCCGTTCTAATTCAGTGGGAGCCGGGGGAAAAATCCTTTCCCAACG
CCCTCCCTGGTCTCTCATCCACAGGGTTCGCCTGATCACCCCTGGGGTACCCTGAATCCCAGTG
TGTCTGGGGAGGTGGAGGCCCTGGGACTGGTTGGGGAACGAGGCCCATGCCACACCCTGAGGGA
ATCTGGGGTATCAATAATCAACCCCAGGTACCAGCTGGGGAAATATTAATCGGTATCCAGGAGG
CAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGGAATATTAATCGGTATCCAGGAG
GCAGCTGGGGGAATATTATCTATACCCAGGTATCAATAACCCATTTCTCCTGGAGTTCTCCGC
CCTCCTGGCTCTTCTTGGAACATCCCAGCTGGCTTCCCTAATCCTCCAAGCCCTAGGTTGCAGTG
GGGCTTAGAGCACGATAGAGGGAAACCAACATTGGGAGTTAGAGTCCTGCTCCCGCCCCCTTGCTG
TGTGGGCTCAATCCAGGCCCTGTTAACATGTTTCCAGCACTATCCCCACTTTTTCAGTGCCTCCCC
TGCTCATCTCCAATAAAATAAAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 64

MQGRVAGSCAPLGILLVCLHLPGLFARSIGVVEEKVSNFGTNLPQLGQPSSTGPSNSEHPQPAL
DPRSNDLARVPLKLSVPPSDGFPPAGGSAVQRWPPSWGLPAMDSWPPEDPWQMAAAAEDRLGEA
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRLPRSNLSLGAGGKILSQRP
PWSLIHRVLPDHPWGTLNPSVSWGGGGPGTGWTRPMPHPEGIWGINNQPPGTSWGNINRYPGGS
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPFPGVLRPPGSSWNIPAGFPNPPSPRLQWG

Important features of the protein:

Signal peptide:

amino acids 1-26

Casein kinase II phosphorylation sites.

amino acids 56-59, 155-158

N-myristoylation sites.

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

FIGURE 65

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTC
TGGGCTGCCCCCTTGTCTCTCTTGACCCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA
CTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCTCCTATGAGTCCAGCTTCTTGGA
TTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCACCATGC
AAGATCTCAACACCATGTTGTCTGCAACACATTGACAGCCATTGAAGCCTGTGTCTTCTTGGCCC
GGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAGCAGGCCCCCACCTC
CTGAGTGGCAATAAATAAAATTCGGTATGCTG

FIGURE 66

MGSGPLPLVLLLTLLGSSSHGTGPGMTLQLKLKESFLTNSSEYESSFLELLEKLCLLLHLPSGTSVTL
HHARSQHHVVCNT

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 37-41

N-myristoylation sites.

amino acids 15-21, 19-25, 60-66

FIGURE 67

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGGGC
CAGGTGCCCCGTGCGAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCC
TTCCTCGGGCGGTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTGCTTCTGGCG
CTGGGGCTGCCGTTCTTGCTGGCCCCGCTGGGGCCGAGCCTGGGGGCAAATACAGACCACTTCTGC
AAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCGTCCGG
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGCTGCCTTGCTCCTGGCTGTGGGGCTG
GCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCCCAGTAGCGA
GGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT
GCCTGCCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAA
GGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAA
AGACTCTGCCCCTGAGGTCAAGAGAGGATGGGGCTATTCACCTTTTATATATTTATATAAAATTAG
TAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

FIGURE 68

MANPGLGLLLALGLPFLRLARWGRAWGQIQTTSANENSTVLPSSSTSSSSDGNLRPEAITAIIVVFS
LLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 56-80

N-glycosylation site.

amino acids 36-40

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 86-90

Tyrosine kinase phosphorylation site.

amino acids 86-94

N-myristoylation sites.

amino acids 7-13, 26-32

FIGURE 69

GCCAGGAATAACTAGAGAGGAACAATGGGGTTATTAGAGGTTTGTCTTCTAGTCTGTGCCTGCTGCACCAG
 TCAAATACTTCTTCATTAAGCTGAATAAATGGCTTTGAAGATATTGTATTGTTATAGATCCTAGTGTGCCAGAA
 GATGAAAAAATAATTGAACAAATAGAGGATATGGTGACTACAGCTTCTACGTACCTGTTGAAGCCACAGAAAAAGA
 TTTTTTTTCAAAAATGTATCTATATTAATTCCTGAGAATTGGAAGGAAAAATCCTCAGTACAAAAGGCCAAAACATGAA
 AACCATAAATGCTGATGTTATAGTTGCACCACCTACACTCCAGGTAGAGATGAACCATACCAAGCAGTTTCAACA
 GAATGTGGAGAGAAAGCGAATACATTCACTTCACCCCTGACCTTCTACTTGGAAAAACAAAATGAATATGGACCA
 CCAGGCCAACTGTTTGTCCATGAGTGGGCTCACCTCCGGTGGGGAGTGTGATGAGTACAATGAAGATCAGCCTTTC
 TACCGTGCTAAAGTCAAAAAAATCGAAGCAACAAGGTGTTCCGCAGGTATCTCTGGTAGAAATAGAGTTTATAAGTGT
 CAAGGAGGCAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACAACAAAATGTATGGAAAAAGATTGTCAATCTTT
 CCTGATAAGTACAAACAGAAAAAGCATCCATAATGTTTATGCAAAAGTATTGATTCTGTTGTTGAATTTTGAACGAA
 AAAACCCATAATCAAGAAGCTCCAAGCCTACAAAACATAAAGTGAATTTTGAAGTACATGGGAGGTGATTAGCAAT
 TCTGAGGATTTTAAAAACACCATACCCATGGTGACACCCTCCTCCACCTGCTCTCATTGCTGAAGATCAGTCAA
 AGAATTGTGTGCTTAGTCTTGTATAAGTCTGGAAGCATGGGGGTAAAGACCGCTAAATCGAATGAATCAAGCAGCA
 AAACATTTCTGTGCTGACAGCTGTTGAAAATGGATCCTGGGTGGGGATGGTTCACTTTGATAGTACTGCCACTATTGTA
 AATAAGCTAATCCAAATAAAAGCAGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGA
 ACTTCCATCTGCTCTGGAATTAATATGCATTTCAAGTGATTGGAGAGCTACATTCCTCAACTCGATGGATCCGAAGTA
 CTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTCTCTGTATGATGAAGTGAACAAAAGTGGGGCCATTGTTTAT
 TTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAAATAGAGATGAGCAAGATAACAGGAGGAAGTCATTTTATGTT
 TCAGATGAAGCTCAGAACATGGCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCAGAGG
 TCCCTTCAGCTCGAAAGTAAGGGATTAACTGAAATAGTAAATGCCTGGATGAACGACACTGTCAATTTGATAGTACA
 GTGGGAAAGGACACGTTCTTCTCATCACATGGAACAGTCTGCCTCCAGTATTTCTCTCTGGGATCCCACTGGGAACA
 ATAATGAAAAATTTACAGTGGATGCAACTTCCAAATGGCCTATCTCAGTATTCAGGAACTGCAAGGTGGGCACT
 TGGGCATACATCTTCAAGCCAAAGCGAACCAGAAACATTAACTATTACAGTAACCTTCTCGAGCAGCAAAATCTTCT
 GTGCCTCCAATCACAGTGAATGCTAAATGAATAAGGACGTAAACAGTTTCCCAAGCCCAATGATTGTTTACGCAGAA
 ATTTCTACAAGGATATGTACCTGTTCTTGGAGCCATGTGACTGCTTTCATTGAATCACAGAATGGACATACAGAAGTT
 TTGGAATTTTGGATAATGGTGACGGCGCTGATTCTTTCAAGAATGATGGAGTCTACTCCAGGTATTTACAGCATAT
 ACAGAAAAATGGCAGATATAGCTTAAAGTTTGGGCTCATGGAGGACAAACACTGCCAGGCTAAAATTACGGCTCCA
 CTGAATAGAGCCGCTACATACCAGGCTGGGTAGTGAACGGGAAATGAAGCAAACCCGCCAAGACCTGAAATTGAT
 GAGGATACTCAGACCACCTTGGAGGATTTCAAGCGAACAGCATCCGGAGGTGCATTTGTGGTATCACAAGTCCCAAGC
 CTTCCCTTGCTGACCAATACCCACCAAGTCAAATCACAGACCTTGATGCCACAGTTTCAAGGATAAGATTATCTT
 ACATGGACAGCACCAGGAGATAATTTTGTATGTTGGAAGGTTCAACGTTATATCATAAGAATAAGTGCAAGTATTCTT
 GATCTAAGAGACAGTTTTGATGATGCTCTTCAAGTAAATACTACTGATCTGTACCAAAGGAGGCCAACTCCAAGGAA
 AGCTTTGCATTTAAACAGAAAATATCTCAGAAAGAAATGCAACCCACATATTTATTGCCATTAAAAATAGATATAA
 AGCAATTTGACATCAAAAGTATCCAACATGCAAGTAACCTTTGTTTATCCCTCAAGCAAATCCTGATGACATTGAT
 CCTACACCTACTCCTACTCCTACTCCTACTCCTGATAAAAGTCATAATTTCTGGAGTTAATATTCTACGCTGGTATTG
 TCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTTAAAGTACCACCATTTGAACCTTAACGAAGAAAAAATCTT
 AAGTAGACCTAGAAGAGAGTTTTAAAAACAAAACAAATGTAAGTAAAGGATATTTCTGAATCTTAAATTCATCCCAT
 GTGTGATCATAACTCATAAAAATAATTTTAAAGATGTCGGAAGAGGATACTTTGATTAAATAAAACACTCATGGATA
 TGTAAAACTGTCAAGATTAAATTTAATAGTTTCATTATTTGTTATTTTGTAAAGAAATAGTGATGAACAAAG
 ATCCTTTTTCATCTGATACCTGGTTGTATATTATTGATGCAACAGTTTTCTGAAATGATATTTCAAATTCATCAA
 GAAATTAATCATCTATCTGAGTAGTCAAAATACAAGTAAAGGAGAGCAATAAACAACATTTGGAAAAAATAA
 AA

FIGURE 70

MGLFRGFVFLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTTASTYLFE
ATEKRFFFEKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEY
IHFTPDLLLKGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCSAGISGRN
RVYKCQGGGCLSRACRIDSTTKLYGKDCQFFPDQVTEKASIMFMQSIDSVVEFCNEKTHNQEAP
SLQNIKCNFRSTWEVISNSEDFKNTIPMVTTPPPPPVFSLLKISQRIVCLVLDKSGSMGGKDRNLN
MNQAAKHFLLOTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGLPTYPLGGTSICSGIK
YAFQVIGELHSQLDGSEVLLLTGDGENTASSCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGG
SHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFL
ITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSR
AANSSVPPITVNAKMNDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGA
GADSFKNDGVYSRYFTAYTENGYSKLVRAHGGANTARLKLRLPPLNRAAYIPGWVVNGEIEANPP
RPEIDEDTQTTLEDFSRASGGAFVVSQVPSLPLPDQYPPSQITDLDATVHEDKIIILTWAPGDN
FDVGKVQRYIIRISASILDRLDSFDDALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAI
KSIDKSNLTSKVSNIQVTLFIPQANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVI
VNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 71

CTCCTTAGTGGAACCCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCGGGAGGGGTGA
CAACAGGTGTCACTTTTTGATCTCGTGTGTGGCTGCCTTCCTATTTCAAGGAAAGACGCCAAGGTAATTTTGACCCA
GAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCAAGTTATGCCAGGATTACTAGAGAGTGTCA
ACTCAACCAAGCAAGCGGCTCCTTCGGCTTAACCTTGTTGGGTTGGAGGAGAGAACCTTTGTGGGGCTGCGTTCTCTAGCA
GTGCTCAGAAGTGACTTGCCTGAGGGTGGACCAGAAGAAAGGATCCCTCTTGTGTTGGCTGCACATCAGGAA
GGCTGTGATGGGAATGAAGGTGAAACTTGGAGATTCACTTCAGTCATTGCTTCTGCCTGCAAGATCATCCTTTAA
AGTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAATCGTTCTAGAAGGAAATGGATGCAAGCAGCTC
CGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCAGGGAAGCCCTTCCGTGGGGGGCCCCGGCTTTGAGGGATGCC
ACCGGTTCTGGACGCATGGCTGATTCTGATGATGTTTCGCCGGGGGCTGCTTGCCTGGATTTCCTGGGTGGTG
GTTTTGCTGGTGTCTCTGCTGTGCTATCTGTCTGTACATGTTGGCTGCACCCCAAAGGTGACGAGGAGCAG
CTGGCACTGCCAGGGCCAACAGCCCCACGGGGAAGGAGGGGTACAGGCGCTCCTTCAGGAGTGGGAGGAGCAGCAC
CGCAACTACGTGAGCAGCCTGAAGCGGCAGATCGCAGAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAAGCAGCTCAGG
AATGGGCAGTACCAAGCCAGCGATGCTGCTGGCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCGACCTC
CTGGCCTTCTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGGCCACAGAGTATGACGAGTG
CCTTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGGCTTACCCGCCACCCGAGGAGAAGCCTGTG
AGGAAGGACAAGCGGGATGAGTTGGTGGAGCCATTGAATCAGCCTTGGAGACCTGAAACAATCTGCAGAGAACAGC
CCCAATCACCGTCTTACAGGCCCTCTGATTTTCATAGAAGGGATCTACCGAACAGAAAGGACAAAGGGACATTGTAT
GAGCTCACCTTCAAAGGGGACCACAAACACGAATTCAAACGGCTCATCTTATTTGACCATTCAGCCCCATCATGAAA
GTGAAAAATGAAAGCTCAACATGGCCAACACGCTTATCAATGTTATCGTGCTCTAGCAAAAAGGGTGGACAAGTTT
CGGCAGTTTCATGCAAGATTTTCAAGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTTACTTTGGG
AAAGAAGAAATAAATGAAGTCAAAGGAATCTTGAACACTTCCAAAGCTGCCAACTTCAGGAACTTTACCTTCATC
CAGCTGAATGGAGAATTTTCTCGGGGAAAGGGACTTGATGTTGGAGCCCGCTTCTGGAAGGGAAGCAACGCTCCTTCTC
TTTTTCTGTGATGTGGACATCTACTTCACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAAG
GTATTTTATCCAGTTCTTTTCAGTCAGTACAATCTTGGCATAATATACGGCCACCATGATGCACTCCCTCCCTTTGGAA
CAGCAGCTGGTGCATAAAGAAGGAAACTGGATTTTGGAGAGACTTTGGATTTGGGATGACGTGTGAGTATCGGTGAGAC
TTCATCAATATAGGTGGGTTTGTCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTTATCGCAAGTATCTC
CACAGCAACCTCATAGTGGTACGGACGCCCTGTGCGAGGACTCTTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAG
CTGACCCCGAGCAGTACAAGATGTGCATGCACTCCAGGCCATGAACGAGGCATCCACCGCCAGCTGGGCATGCTG
GTGTTCAGGCACGAGATAGAGGCTCACCTTCGCAAAACAGAAACAGAAAGCAAGTAGCAAAAAACATGAACCTCCCA
GAAGGATTGTGGGAGACACTTTTCTTTTCCCTTTTGCATTAATCTGAAAGTGGCTGCAACAGAGAAAAGACTTCCATAAA
GGACGACAAAAGAAATGGACTGATGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTGTGGGCTTTTACAAACAGA
AATCAAAATCTCCGCTTTGCTGCAAAAGTAACCCAGTTGCACCCTGTGAAGTGTCTGACAAAGGCAGAAATGCTTGTG
AGATTATAAGCCTAATGTTGTGGAGGTTTTGATGGTGTTCATAATACACTGAGACCTGTTGTTTTGTGTGCTCATTGA
AATATTCTAGTTTAAAGCAGTTTGTGAAAAATTCATTAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGA
GCCTATCAGCAGGGCTCTAGTTTCTAGGAATGCTAAAAATATCAGAAGGCAGGAGAGAGATAGGCTTATTATGATACT
AGTGAGTACATTAAGTAAATAAAATGGACAGAAAAGAAAAGAACCAATATATCGTGTCAATTTTTCCCCAAGAT
TAACCAAAAATAATCTGCTTATCTTTTGGTTGTCCTTTTAACTGTCTCCGTTTTTTCTTTTATTTAAAAATGCACT
TTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTACCACTTTGCAAGCCTTACAAGAGAGCACAAGTTGGCCTAC
ATTTTTATATTTTTTAAAGATACTTTGAGATGCATTATGAGAACTTTCAGTTCAAAGCATCAAATGATGCCATAT
CCAAGGACATGCCAAATGCTGATTCTGTGAGGCACTGAATGTGAGGCACTGAGACATAGGGAAGGAATGGTTGTACT
AATACAGACGTACAGATACTTTCTGGAAGATATTTTGAAGAGGCAACTGAACACTGGAGGAAAAGAAAATGAC
ACTTTCGCTTTACAGAAAAGGAACTCATTGAGACTGGTGATATCGTGATGTACCTAAAAGTCAAGAACCACTTTT
CTCCTCAGAAGTAGGACCGCTTCTTACCTGTTTAAATAAACCAAGTATACCGTGTGAACCAAAACATCTCTTTT
AAAACAGGGTGTCTCCTGCTTCTGGCTTCCATAAGAAGAAATGGAGAAAATATATATATATATATATATATTTGT
GAAAGATCAATCCATCTGCCAGAACTAGTGGGATGGAGTTTTTGTACATGTTATCCACCCAGGCCAGGTGGAAG
TAACTGAATTATTTTTTAAATTAAGCAGTTTACTCAATCACAAGATGCTTCTGAAAATTGCATTTTATTACCATTT
CAAATATTTTTTAAAAATAAACAGTTAAACATAGAGTGGTTTTCTTATTGATGTGAAAATTATTAGCCAGCACCAG
ATGCAATGAGCTAATTATCTCTTTGAGTCTTGTCTGTTTGTCTCACAGTAAACTCATTGTTTAAAGCTTCAAGAAC
ATTCAAGCTGTTGGTGTGTTAAAAATGCATTGTATTGATTTGTACTGGTAGTTTATGAAATTTAATTAAAAACACAGG
CCATGAATGGAAGGTGGTATTGCACAGCTAATAAAATATGATTTTGGATATGAA

FIGURE 72

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEW
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDK
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETNNPA
ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVNEKLNMAN
TLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNF
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNLCRLNTQPGKKVFYPVLSQY
NPGIYYGHDAVPPLQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGEDVHLYR
KYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHL
RKQKQKTSSKKT

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 315-319, 324-328

N-myristoylation sites.

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

Amidation site.

amino acids 377-381

FIGURE 73

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGATCCA
GAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACAGCAAGA
GAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTCTCACTCCTC
CCTCCCTCTCTCTCTGCTGTCTAGTCTCTAGTCTCTCAAATCCCAGTCCCCTGCACCCCTTC
CTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCCTGGCTGCAGATGGGG
GTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCAGCCTCTTACCCTGAGTGT
GGAAACAATGCCAGTCGCCCATCGATATTCAGACAGACAGTGTGACATTTGACCCTGATTTGCC
TGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCAGCCTTTGGACCTGCACAACAATGGCC
ACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCT
GCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGGTGAGAACACCAGATCAACAG
TGAAGCCACATTTGCAGAGCTCCACATTGTACATTATGACTCTGATTCTATGACAGCTTGAGTG
AGGCTGCTGAGAGGCTCAGGGCCTGGCTGTCTGGGCATCCTAATTGAGGTGGGTGAGACTAAG
AATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTC
AGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAACAGCTGGGGCAGTACTTCCGCTACAATG
GCTCGCTCACAACCTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAG
ATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAA
GCTTCTGGTACAGAACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCA
TCCAAGCAGGATCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTGGC
TGTCTCTGCCTTCTCTGGCTGTTTATTTTATTGCTAGAAAGATTGGAAGAAGAGGCTGGAAAA
CCGAAAGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATAC
CATGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGG
CCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAGGAAT
GGACCCAGGCTGTCAATCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAA
ATGAGGAAATCGCTGTGTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGGGAAGTTGGG
ATATACCCCAAAGTCCTCTACCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGGGATCT
CTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTGTATCAATATATTTGGAAATTAAG
TTTCTGACTTT

FIGURE 74

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPDLPALQ
PHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGGSEHQINSEAT
FAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP
FNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLV
QNYRALQPLNQRMVFAFIQAGSSYTTGEMLSLGVGILVGCCLLLAVYFIARKIRKKRLENRKS
VVFTSAQATTEA

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 75

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCCCTTGGGGACGGGCAGTTCCTGTGTCT
TCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGTCCTACA
ATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTTCATCACAA
ATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTGACAGCTCC
AGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCTGA
AGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAACCAC
ACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCCTTCGTCCC
AGGGCCCCCTCGCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGATCAATCAT
CAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGTGTTCCTTTTT
TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACACCCAGCAAATTT
GATTTTGATTTATGAAATGAATTTGACAAAAGATTCTTTGTGCCTGTGAAAAATCGTGATTA
ACTTTATCACCCCTCAATATCTCGGATGATTCTAAATTTCTCATCAGGATATGAGTTTACTGGGA
AAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGA
GGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGAAATTTTTGTGACTCTGAAG
AAAACACGGAAGGTACTTCTCTACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCCGGATAAA
ACAGTCATTGAATATGAATATGATGTGAGAACCCTGACATTTGTGCGGGGCTGAAGAGCAGGA
GCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAG
TCTTGGGCCCCGAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCG
CAGGAGCACACAGACTCGGAGGAGGGGCGGAGGAAGAGCCATCGACGACCTGGTTCGACTGGGA
TCCCCAACTGGCAGGCTGTGTATTCTTCGCTGTCCAGCTTCGACCAGGATTGAGAGGCTGCG
AGCCTTCTGAGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCT
CCAGACAGGCCACCAGGAGAAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGTTATA
TGTGCAGATGGAAACTGATGCCAAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAACAAGTGAG
TCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTGAGTGT
CTGTGAGAATTACTTATTTCTTTCTCTATTCTCATAGCACGTGTGTGATTGGTTTCATGCATGTA
GGTCTCTTAACAATGATGGTGGGCTCTGGAGTCCAGGGGCTGGCCGGTTGTCTATGCAGAGAA
AGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGGTGGGTGT

FIGURE 76

MSYNGLHQRVFKELKLLTLCSSIQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIY
SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLK
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYIGNEFDKRFFVPAEK
IVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFC
DSEENTEGTSLTQQESLSRTIPDKTVIEYDYVRTTDICAGPEEQELSLQEEVSTQGTLLESQA
ALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPPSTTLVDWDPQTGRLCIPSLSSFDQDS
EGCEPSEGDGLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 77

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACAC
CTGGGAAGATGGGCCGGCCCGTGGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATC
CAAGCCACCCTCAGTCCCACTGCAGTTCTCATCCTCGGCCCAAAGTCATCAAAGAAAAGCTGAC
ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC
GGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCCTGAAGCACATC
ATCTGGCTGAAGGTATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTCGGCCAATGACCA
GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCCTGGTCAAGACCA
TCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGATGGACACCAGTGCAAGTGGC
CCCACCCGCCTGGTCTCAGTGAAGCTGTGCCACCAGCCATGGGAGCCTGGCATCCAAGTCTGTA
TAAGCTCTCCTTCTGGTGAAGCCTTAGCTAAGCAGGTATGAACCTCCTAGTGCCATCCCTGC
CCAATCTAGTGAAAACAGCTGTGTCCCCTGATCGAGGCTTCCTTCAATGGCATGTATGCAGAC
CTCCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTA
TCCTGCCATCAAGGGTGACACCATTAGCTCTACCTGGGGGCCAAGTTGTGGACTCACAGGGAA
AGGTGACCAAGTGTTCAATAACTTCGAGCTTCCCTGACAATGCCACCCTGGACAACATCCCG
TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA
ATTCATGGTCTGTTGGACTCTGTGCTTCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGC
TGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGAC
ACTCCCGAGTTTTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTT
TCCCTCCAGTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGT
TTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTG
ATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA
CTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTGAAGG
CCTTGGGATTGCAGGCAGCTGAGTCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCC
TTGTGGAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGATGGCAGCCATCAGGGAAGGCTGG
GTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTG
CCTGTGAAAAA

FIGURE 78

MAGPWTFLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQLPLLSAMREK
PAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITQLYLGAKLLDSQGKVT
KWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPPEEFMVLLDSVLPESAHLKSSIGLIN
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSALRPLFTLGIEASSEAQFYT
KGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIHSILLPNQNGKLRSQVPSLVKALG
FEAAESSLTKDALVLTASLWKPSSPVSQ

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 79

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC
TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCT
CTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGTTGCCAT
GCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAGCAGTTGGCTTCT
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGACATCTATAGC
ACCCTTCTGGGCCTGCCCCGCTGACATCCAGGCTGCCCAGGCCATGATGGTGACATCCAGTGCAAT
CTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCCAGGAATCCC
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTCATCCTTGGAGGCCTCCTGGGATTC
ATTCTGTTCCTGGAATCTTCATGGGATCCTACGGGACTTCTACTCACCAGTGGTGCCTGACAG
CATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTCTCCCTGTTCTCCCTGATAG
CTGGAATCATCCTCTGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACTACTACGATGCCTAC
CAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGA
GTTCAATTCCTACAGCCTGACAGGGTATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGTGGCTG
GGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGT
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGCATTGAGCAAAGGCAGAAATGGGG
GCTAGTGTAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCC
TCACCTTGCTGCTCCCCTGCCCTAAGTCCCCAACCCCTCAACTGAAACCCCATTCCTTAAGCCA
GGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACA
TCCCCTGACTGACCCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATT
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTC
CCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCCTCTGTTATGACTCCACAGTGTCCA
GACTAATTTGTGCATGAAGTGAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATG
CAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

FIGURE 8o

MASLGLQLVGYYLGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD
IYSTLLGLPADIQAAQAMMTSSAIISSLACIIISVGMRICTVFCQESRAKDRVAVAGGVFFILGGL
LGFIPVAWNHLHGILRDFYSPVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQQRNRSNYY
DAYQAQPLATRSSPRPGQPPKVKSEFNYSYSLTGYV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 81

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTC
CCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCCTGCCCTCCTTTTCCT
GCCCACCGCTGCTTCTTGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGG
GTTGATCTGTGGCCCTGTGCCTCCGTGTCCTTTTCGTCTCCCTTCCTCCCGACTCCGCTCCCGG
ACCAGCGGCCTGACCCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCTCTCCTCCTTGCTGGGA
CTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCAGACATGTTCTGCCTTTT
CCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGT
ACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCT
GTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACAC
TCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCCAGCACAACGGGACCATGTACCAACACGGAG
AGATCTTCAGTGCCCATGAGCTGTTCCCTCCCGCTGCCCAACCAGTGTGTCTCTGCAGCTGC
ACAGAGGGCCAGATCTACTGCGGCCTCACAACTGCCCGAACCAGGCTGCCAGCACCCCTCCC
ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACA
GTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGTGGGAGAAAG
AGAGGCCCCGGGCACCCAGCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT
CAGACCCAAGGGAGCAGGCAGCACAAGTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCT
GTGTGCATGGCGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC
CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC
CACCGAGTACCCCTGCCGTACCCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTTGCCAGAGG
ACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTC
CTCGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGC
CTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAAACTGAGGCTCAGAGAG
GTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGAATCAGATCAAGAAAGTCAG
GAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCACGAAGGTCACT
GGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAG
ACATAACAAAGACCTAAACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATAATAAA
TAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 82

MVPEVRVLSSLLGLALLWFLDSSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRTCSE
GAHVSCYRLHCPVHCPQPVTEPQCCPKCVPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELF
PSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR
HPQDPCSSDAGRKRGPPTAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKHKKACVHGGKTYS
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTTEYPCRHPKAGKCKICPEDKADPGHSE
ISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH
SQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSDPGAEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

FIGURE 83

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGGCCCTCCGCTCACGCAGAGCCTCTCC
GTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCATCCGTCACCTCTCCTGTCA
TCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTTGGTTCTGAGTC
TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTTGGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAG
GACGCAGCATTCTCCTGTTTCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAGTGGCGTTCTTCAGGGG
CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATC
AAGGCAGGACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTACT
GTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCATCTGGGAGCT
ACAGGTGTGAGCACTGGGCTCAGTTCTCTCATTTCATCACGGGATATGTTGATAGAGACATCCAGCTAC
TCTGTCACTCCTCGGGCTGGTTCCCCCGGGCCACAGCGAAGTGGAAAGGTCCACAAGGACAGGATTTGTCC
ACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTTGTATGTGGAGATCTCTCTGACCGTCCAAGAGAA
CGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAG
GAGATACTTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTA
TTTTTTGGCATTGTTGACTGAAGATTTTCTTCTCCAATTCCAGTGGAAAATCCAGGCGGAACTGGACTG
GAGAAGAAAGCACGGACAGGCAGAAATTGAGAGACGCCCGAAACACGCAGTGGAGGTGACTCTGGATCCAG
AGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAATGTAACCCATAGAAAAGCTCCCCAGGAGGTG
CCTCACTCTGAGAAGAGATTACAAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAGGGAACATTA
CTGGGAGGTGGACGGAGGACACAATAAAAGGTGGCGGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGA
AGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTTC
ACATTAAATCCCCGTTTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTCTGGACTA
TGAGTGTGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTGCGTTTG
AAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCCCATAGTCATCTGC
CCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGCAATCCCAGAGACAAGCAACAG
TGAGTCTCTCTCACAGGCAACCACGCCCTTCTCCCCAGGGGTGAAATGTAGGATGAATCACATCCCACAT
TCTTCTTTAGGGATATTAAGGTCTCTCTCCCAGATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCA
GATGAAGGGGGACTGGCCTGTCCACATGGGAGTCAGGTGTCTGCTGCCCCTGAGCTGGGAGGGAAGAAGG
CTGACATTACATTTAGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAG
AACCGTCAGGAATCCCATCTCACAGGCTGTGGTGTGATTAAAGTAGACAAGGAATGTGAATAATGCTTAG
ATCTTATTGATGACAGAGTGTATCCTAATGTTTGTTCATTATATTACACTTTCAGTAAAAAAA

FIGURE 84

MAIMLSLVLSLLKLGSGQWQVFGPDKPQALVGEDAAFSCLSPKTNAEAMEVRFFRGQFSSVH
LYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQKAIWELQ
VSALGSVPLISITGYVDRDIQLLCQSSGWFPPTAKWKGPQGDLSTDSRTNRDMHGLFDVEISL
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK
FQWKIQAELDWRRKHGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF
TRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRKEYVTLSPDHGYWVLRNLGEHLYFT
LNPRFISVFPRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT
PIVICPVTQESEKEASWQRASAIPTSNSSESSQATTPFLPRGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

[illegible][illegible]

FIGURE 86

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFYPSHGWYIPGPVVHGYWFREG
ANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNY
KHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPWACEQGTTPMISWIGTSVSPDPSTTRS
SVLTLIPQPDHGTSLTCQVTFPGASVTNKTVHLNVSYPQNLMTVTFQGDGTVSTVLGNGSSL
SLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP
LGSQQVYLNVSLSKATSGVTQGVVGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGDGTGIE
DANAVRGSASQGPLETPWAEDSPPDQPPASARSSVGEGELQYASLSFQMVKPWDSRGQEATDTE
YSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 87

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTAC
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAAATGAACCAACTCAGCTTCCTGCTGTTTC
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT
TCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCATTGA
TGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCTGTGACATGACCTCTG
GGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGGAAGTGCACGGTG
GGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAACTGGGC
CAACTACAACACCTTTGGATCTGCAGAGGGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACT
ACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCCAATAAGTCCCCATGCAGCACTGG
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCT
GTTTGGCATCTACCAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC
CGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCCAGAAAACAGCATCTTATTACTCACCTTAT
GGCCAGCGGGAATTCAGTGCGGGATTTGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAA
CGCCTTGTTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG
GATACTTTCCAGAGGCCAGTCCCCAGCAGTGIGGAGATTTTCTGGTTTTGATTGGAGTGGATAT
GGAACATCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG
TTGAGAGTTTTGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAA
CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGA
AAAAAA

FIGURE 88

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI
YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAAT
SDDYKNPGYYDIQAKDLGIWHPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYG
EGKCWTDNGPVI PVVYDFGDAQKTASYSPYQREFTAGFVQFRVFNNERAANALCAGMRVTGCN
TEHHCIGGGGYFPEASPPQCDFSGFDWSGYGTHVGYSSSREITEAAVLLFYR

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation site.

amino acids 163-167

Glycosaminoglycan attachment sites.

amino acids 74-78, 289-293

N-myristoylation sites.

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

FIGURE 89

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGAGAC
CGCCGCCCTTGTCCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCTGACG
CTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTG
CCTGCCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTTCAGCTGGTGGCCGCGCTCT
CTGTCACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCTCTCAGGAGTCTCCATGTTCAAC
AGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGCCCTGTCCTTCTTCAT
ATTTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCTTCTGCAGTGCCCTTCCAGCTG
TCACTGAAATGGCTTTATTCGTCACCGTCTTTGGGCTGAAAAAGAAACCCTTCTTGATTACCTTCA
TGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCCTGGAAGAAGGAAG
GCATAGGCTTCGGTTTTCCCCTCGGAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACG
TCTTGAGTCTGGGATTATCCGCATTGTATTTAGTGCTTTGTAATAAAATATGTTTTGTAGTAACA
TTAAGACTTATATACAGTTTTAGGGGACAATTAAAAAAAAAAAA

FIGURE 90

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFA
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVTEMALFV
TVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 91

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC
TCGCTGCTGCTTCGTGTTCTTGGTGCAGGGTAGCCTCTATCTGGTCACTCTGTGGCCAGGATGATG
GTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCT
CGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCTCCTAGGGCTGCT
GGCCCCGCTTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCCCGAACCACAGCCCCC
CACCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCCAACATCAAGACGGTG
GCCCTGAACCTGCTCGTCACAGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTCCACTT
CCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAG
AGTTCACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCTCCAAAATCTTCAACTGCCGGATG
GAGTGGGAGAAGGTAGAACGGGGCCCGGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTG
CTCCCGAGACCAGCTCAGAGCTCAGCCACCTGGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTG
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCAGATTACAACCTAC
CATAGTGATACCCCCTACTACCCATCTGGGTGACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGC
TGGAAGGACAGGCCTGCCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGGCTC
AGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG
AGAAAGGGTCCCAAGTGTGCTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGG
AGGAGGAGTGGGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGG
TCCCCGAGGCCTGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGC
CCTTGGTTCTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTCATCAGTGTGGACA
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGG
GCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCTTGTCGTGTGCTGAGCATGG
CATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC
CAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG
GCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCCACAGCCCATC
CGCGTGCTGTGTGCCCTCTTCCACCCCAACCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCG
GAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGTTCTCCCGATCTGGATGGCGC
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCGGGCCGAGAGCATGTGCTGGATCTGTTT
TGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGTGAAACCGCTGATTGCTGACTTT
TGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAAGCTTGCCCCGGGGCA

FIGURE 92

MQLTRCCFVFLVQGSLLYVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL
LGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTF
SVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDP
AKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPSG

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 93

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCGCC
CTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGAGCTTTCTT
CTGGTTGGTGTCTCTACTGATTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTATTGACAACA
AAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTGTCTATATCCAAGAA
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTTGAAGAGTATAAACCC
AGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGGGCTTTGGAATCATGA
GTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCATTCTAT
GGAGATTCTCCTCAATTCTTCCTTTATTTCAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGT
ATTCTGGGGCATTGTATTTTTTGTATGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTC
TCCTGACCCACCTGCTGGTGTCTAGCCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCG
TCAGCATTTATAATCCTGGTGTCTATGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCG
AAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGAT
AACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCT
TTTTCTGAAAATCCCTTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 94

MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG
PTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV
FSFVNTLSDSLGPGTVGIGHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVLLT
HLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKCLLCQDKNFLLYNQRSR

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 95

AATTTTTCACCAGAGTAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTGCCTCGTG
GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTGTCTTCTAGGATCAAC
TCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACCTGGCTCCGGATCAGG
GAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTGATACCATTAAACA
CAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACACCTGGTAC
CCAGACCCACCCATTGACCCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTTAC
CAATTTTGTACACAACCTTGGAGCCCAGGGCACTATCCTAAGCTCAGAGGAATTGCCACAAATC
TTCACGAGCCTCATCATCCATTTCCTTGTTCCCGGGAGGCATCTGCCACCAGTCAGGCAGGGGC
TAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAGGAGCAGGTGTAAATCCTGCCACCCAGG
GAACCCAGCAGGCCGCTCCCAACTCCCAGTGGCACAGATGACGACTTTCAGTGACCACCCCT
GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA
GTAAGCTGTTTCAAATTTTTTCAACTAAGCTGCCTCGAATTTGGTGATACATGTGAATCTTTATC
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATT
TACCTGAAAATATTCTTGAAATTCAGAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAA
CAATAATTCAATGGATAAATCTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATAT
TAAACATATTTGGAAAACCTGGAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 96

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQOQSNQVFPSSLSLIPTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE
LPQIFTSLIIHSLFPGGIILPTSQAGANPDVQDGLSPAGGAGVNPATQGTAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 97

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT
 CTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTGACCATG
 GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGCCAGCCTGC
 AGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAATTTCCCTTTATACCTGACCAAGTTGC
 CGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTGAGGGGACTCAGGCAAGGCAACTGAG
 GGCCCATTTGCTATGGATCCAGATTCTGGCTTCTGTGCTGGTGACCAGGGCCCTGGACCCGAGAGGA
 GCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATGGACATGTCTTGTGGGGTCCAC
 AGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTGCCCCATTTCTCTCAAGCCATCTAC
 AGAGCTCGGCTGAGCCGGGGTACCAGGCCCTGGCATCCCCTTCTCTTCTTCTGAGGCTTCAGACCG
 GGATGAGCCAGGCACAGCCAACTCGGATCTTCGATTCCACATCCTGAGCCAGGCTCCAGCCCAGC
 CTTCCCCAGACATGTTCCAGCTGGAGCCTCGGCTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGC
 ACCAGCCTTGACCACGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGA
 CCAGGCCTCAGGCCACCCAGGCCACTGCCACCGTGGAGGTCTCCATCATAGAGAGCCTGGGTG
 CCCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCTTATACCCGCAACCATGGCCAGGTA
 CACTGGAGTGGGGGTGATGTGCACTATCACCTGGAGAGCCATCCCCGGGACCTTTGAAGTGAA
 TGCAGAGGGAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCC
 AGGTGCGGGCTCAGAATTCCTATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTG
 ATGGATGAGAATGACAACGTGCCATCTGCCCCCTCGGCTGACCCACAGTCAGCATCCCTGAGCT
 CAGTCCACCAGGTACTGAAGTGACTAGACTGTCAGCAGAGGATGCAGATGCCCCGGCTCCCCCA
 ATTCCACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGGCCTTC
 CAGGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACAT
 CCTGCTTCTGGTGTGCGCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGTGAAG
 TCGAAGTCGAGTACAGATATCAATGATCAGCCCCCTGAGTTCATCACTTCCCAGATTGGGCCT
 ATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCATTGATGCTGA
 CCTCGAGCCCGCCTTCGCGCTCATGGATTTTGCCATTGAGAGGGGAGACAGAAAGGACTTTTG
 GCCTGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG
 GCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGGCCAGGCC
 AGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGAGTGTGCCACCCCCCAAGTTGG
 ACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCCAGCCGGCTCTTCTCTGCTGACCATC
 CAGCCCTCCGACCCCATCAGCCGAACCCCTCAGGTTCTCCCTAGTCAATGACTCAGAGGGCTGGCT
 CTGCATTGAGAAATTTCTCCGGGGAGGTGCACACCGCCAGTCCCTGCAGGGCGCCAGCCTGGGG
 ACACCTACACGGTGCTTGTGGAGGCCAGGATACAGCCCTGACTCTTGCCCTGTGCCCTCCCAA
 TACCTCTGCACACCCCGCCAAGACCATGGCTTGATCGTGAGTGGACCCAGCAAGGACCCGATCT
 GGCCAGTGGGCACGGTCCCTACAGCTTCACCCCTTGGTCCCAACCCACGGTGCAACGGGATTGGC
 GCCTCCAGACTCTCAATGGTTCCCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCAGT
 GAACACATAATCCCGTGGTGGTGCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGAT
 CGTGTGCTGCTGCAACGTGGAGGGGAGTGCATGCGCAAGGTGGGCGCATGAAGGGCATGCCCA
 CGAAGCTGTGCGCAGTGGGCATCCTTGTAGGCACCCTGGTAGCAATAGGAATCTTCCTCATCCTC
 ATTTTACCCACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCT
 GAAGGGGACTGTCTGAATGGCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAG
 TCCCCCTGGGAGAGGCCAGCACCCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCTCCA
 TCTGCCCTGGGGTGGAGGCCACCATCACCATCACAGGCATGTCTGCAGAGCCTGGACACCAACTT
 TATGGACTGCCCATGGGAGTGCTCCAAATGTCAGGGTGTGTTGCCCAATAATAAAGCCCCAGAGAA
 CTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 98

MVPAWLWLLCVSPQALPKAQPAELSVPEVNYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT
EGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVPHFSQAI
YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRLGALALSPKG
STSLDHALERTYQLLVQVKMDGQASGHQATATVEVSI IESTWVSLEPIHLAENLKVLYPHHMAQ
VHWSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQNSHGEDIAAPLELHVL
VMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSHVYQLLSPEPEDGVEGRA
FQVDPTSGSVTLGVPLRAGQNILLVLAMDLAGAEGGFSSTCEVEVAVTDINDHAPEFITSQIG
PISLPEDVEPGTLVAMLTADADLEPAFRLMDFAIERGDTEGTFGLDWEPDSGHVRLRLCKNLSY
EAAPSEHVVVVVQSVAKLVGPGPGGATATVTVLVERVMPPPKLDQESYEASVPISAPAGSFLLT
IQPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALT LAPVPS
QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGPNTVQRDWRLQTLNGSHAYLT LALHWVEP
REHIIPVVVSHNAQMWQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGT LVAIGIFLI
LIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 99

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCCACGCCCTG
AGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTA
TCTCTTCACCTTCAAGTCCCCTTTCTCAAGAATCCTCTGTCTTTGCCCTCTAAAGTCTTGGTAC
ATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG
TTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCCAATGAGACTAGCACC
TCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCACCAACTCTGGGTCCAG
TGTGACCTCCAGTGGGGTCAGCACAGCCACCCTCTCAGGGTCCAGCGTGACCTCCAATGGGGTCA
GCATAGTCACCAACTCTGAGTTCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG
TTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGG
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCCTCCAGTGGGGCCAGCACAGTCCACCAACT
CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCC
AGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCAC
CAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA
CCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACT
GCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG
AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGGGGCCA
GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAG
TCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG
GGCTAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACT
CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCCACCAATTCTGAGTCCAGCACACCCTCC
AGTGGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAACACAGCCAC
CAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAA
CCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACA
GCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCTAG
CACAGTGTCCAGTGGGATCAGCACAGTCCACCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCA
ACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGA
ATGCACACAACTTCCCATAGTGCATCTACTGCAGTGTGAGGCAAAGCCTGGTGGGTCCCTGGT
GCCGTGGGAAATCTTCTCATCACCTTGGTCTCGGTGTGGCGGCCGTGGGGCTCTTTGCTGGGC
TCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGTCTACACCCT
CATGGCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCACAGGCCAG
GTGGAGTCCTAACCTGGTCTGGAGGAGACCAGTATCATCGATAGCCATGGAGATGAGCGGGAGGA
ACAGCGGGCCCCTGAGCAGCCCCGGAAGCAAGTGGCGCATTCTTCAGGAAGGAAGAGACCTGGGCA
CCCAAGACCTGGTTTCTTTTATTTCATCCAGGAGACCCCTCCAGCTTTGTTTGAGATCCTGAA
AATCTTGAAGAAGGTATTCTCACCTTTCTTGCCTTTACCAGACACTGGAAAGAGAATACTATAT
TGCTCATTTAGCTAAGAAATAAATACATCTCATTAACACACAGACAAAGAGAAGCTGTGCTTG
CCCCGGGTGGGTATCTAGCTCTGAGATGAATCAGTTATAGGAGAAAACCTCCATGCTGGACTC
CATCTGGCATTCAAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 100

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATISGS
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNESSTTSSGASTATNESSTPSS
GASTVTNSGSSVTSSGASTATNESSTVSSRASTATNESSTLSSGASTATNSDSSTTSSGASTA
TNSESSTTSSGASTATNESSTVSSRASTATNESSTTSSGASTATNESRRTTSNGAGTATNES
STTSSGASTATNSDSSTVSSGASTATNESSTTSSGASTATNESSTTSSGASTATNSDSSTTSS
GAGTATNESSTVSSGISTVTNESSTPSSGANTATNESSTTSSGANTATNESSTVSSGASTA
TNSESSTTSSGVSTATNESSTTSSGASTATNSDSSTTSSEASTATNESSTVSSGISTVTNES
STTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVA
AVGLFAGLFFCVRNLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAPHRPRWSPNWFWRPVSII
AMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 101

GGCCGGACGCTCCGCGTTACGGGATGAATTAACGGCGGGTTCGCGACGGAGGTTGTGACCCCTA
CGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGGGCGTGCCCTGCTTGTCACAGGTG
GGAGGCTGGAACATACAGGCTGAAAAACAGAGTGGGTACTCTTCTGGGAAGCTGGCAACAAAT
GGATGATGTGATATATGCATTCCAGGGGAAGGAAATTGTGGTGCTTCTGAACCCATGGTCAATT
AACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCTTTGGAATCAT
GGTGTGATGGAAGGGATTTACTTTATACTGACTCTGTTTTGGGAAGCTTTTTTGGAGCATT
TCATGCTGAGTCCCTTTTTTACCTTTGATGTTTGTAAACCCATCTTGGTATCGCTGGATCAACAAC
CGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCATGTTTGGTGTAAAGT
GATTATAACTGGGGATGCATTTGTTCTCGGAGAAAGAAGTGTGATTATCATGAACCATCGGACAA
GAATGGACTGGATGTTCTGTGGAATTGCCTGATGCGATATAGCTACCTCAGATTGGAGAAAATT
TGCCTCAAAGCGAGTCTCAAAGGTGTTCTCGGATTTGGTTGGGCCATGCAGGCTGCTGCCATAT
CTTCATTCATAGGAAATGGAAGGATGACAAGAGCCATTTTGAAGACATGATTGATTACTTTTGTG
ATATTCACGAACCACTTCAACTCCTCATATTTCCAGAAGGGACTGATCTCACAGAAAACAGCAAG
TCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTCAGAAATATGAATATGTTTTACATCCAAG
AACTACAGGCTTTACTTTTGTGGTAGACCGTCTAAGAGAAGGTAAGAACCTTGATGCTGTCCATG
ATATCACTGTGGCGTATCCTCACACATTCCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTTT
CCCAGGGAAATCCACTTTTACGTCCACCGGTATCCAATAGACACCTCCCCACATCCAAGGAGGA
CCTTCAACTCTGGTGCCACAAACGGTGGGAAGAGAAAGAAGAGAGGCTGCGTTCCTTCTATCAAG
GGGAGAAGAATTTTTATTTTACCGGACAGAGTGTGATTCCACCTTGCAAGTCTGAACTCAGGGTC
CTTGTGGTCAAATTGCTCTCTATACTGTATTGGACCCTGTTTCAGCCCTGCAATGTGCCTACTCAT
ATATTTGTACAGTCTTGTTAAGTGGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGA
GAATATTTGGTGGACTGGAGATCATAGAACTTGCATGTTACCGACTTTTACACAAACAGCCACAT
TTAAATTCAAAGAAAAATGAGTAAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTG
GAAATGTTCTAAACCTTTCTAAGCTCAGATGCATTTTGCATGACTATGTCGAATATTTCTTACT
GCCATCATTATTTGTTAAAGATATTTTGCACCTAATTTTGTGGGAAAAATATTGCTACAATTTTT
TTAATCTCTGAATGTAATTTTGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTT
GGGCCAGAATATTATTAAACAATCATCAGGCTTTTTAAA

FIGURE 102

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSGIMVSWKGIYFILTLFWGSFFGSIFMLSP
FLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM
FLWNCLMRYSYLRLEKICLKASLKGVPFGFWAMQAAAYIFIHRKWDDKSHFEDMIDYFCDIHEP
LQLLIFPEGTDLTENSKSRSNFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLDAVHDITVA
YPHNIPQSEKHLQGDFFPREIHFFVHRYPIDTLPTSKEQLQWCHKRWEEKEERLRSFYQGEKNF
YFTGQSVIPPCKSELRLVLVVKLLSILYWTLFSPAMCLLIYLYSLVKWYFIITIVIFVLQERIFGG
LEIIEELACYRLHKKQPHLNSKKNE

Important features of the protein:

Signal peptide:

amino acids 1-22

Transmembrane domains:

amino acids 44-63, 90-108, 354-377

FIGURE 103

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGACC
TCCAAATCATCCATCCACCCCTGCTGTCTATCTGTTTTTCATAGTGTGAGATCAACCCACAGGAATA
TCCATGGCCTTTTGTGCTCATTITGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTGGCAAGT
CACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTGCTCCCTCT
TTCCTGAGACCACTGCAGAGGCTATGGAAGTGCAGTTTCTCAGGAATCAGTTCATGCTGTGGTC
CACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAACTGA
GTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGCTAAAAACATCACTCCCTCGG
ACATCGGCCTGTATGGGTGCTGGTTTCACTTCCAGATTTACGATGAGGAGGCCACCTGGGAGCTG
CGGGTGGCAGCACTGGGCTCACTTCTCTCATTTCATCGTGGGATATGTTGACGGAGGTATCCA
GTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGCCACAGCCAAGTGAAAGGTCCACAAGGAC
AGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGATGTGGAGATCTCC
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGA
GGTGAATCCAAGGTATTGATAGGAGAGACGTTTTTCCAGCCCTCACCTGGCGCCTGGCTTCTA
TTTTACTCGGGTTACTCTGTGGTGCCCTGTGGTGTGTCATGGGGATGATAATTGTTTTCTTC
AAATCCAAAGGGAAAATCCAGGCGGAACTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAG
AGACGCCCGGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCG
TTTCTGATCTGAAAATGTAACCATAGAAAAGCTCCCCAGGAGGTGCCCTCACTCTGAGAAGAGA
TTTACAAGGAAGAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGA
CGTGGGACAAAATGTAGGGTGGTATGTGGGAGTGTGTGGGATGACGTAGACAGGGGGAAGAACA
ATGTGACTTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTT
ACATTCAATCCCCATTTTATCAGCCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCCT
GGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGC
TGACATGTGAGTTTGAAGGCTTGTGAGACCTATATCCAGCATGCGATGTATGACGAGGAAAAG
GGGACTCCCATATTTCATATGTCCAGTGTCTGGGGATGAGACAGAGAAGACCCTGCTTAAAGGGC
CCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGCCCCAGCTTCCTCT
CCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCC
TGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCTGTGGGAG
TCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAA
CTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCCCAGGCTCCTCATTGCTAGTCACGG
ACAGTGATTCTGCTCAGAGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGCAGGTT
TGAGGGCACAGTGTGCTAATGATGTGTTTTATATTATACATTTTCCACCATAAACTCTGTT
TGCTTATTCACATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACACC
TGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTCACTGATTCTATAAGCCCAGCAT
TACCTGATACCAAAACCAGGCAAGAAAACAGAAGAAGAGGAAGGAAAACACAGGTCCATATCC
CTCATTAACACAGACACAAAAATCTAAATAAAATTTAACAATTAACATAAACAATATATTTA
AAGATGATATATACTACTCAGTGTGGTTTGTCCACAAATGCAGAGTTGGTTTAATATTTAAAT
ATCAACCAGTGAATTCAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAAAAAAAAAAA

FIGURE 104

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH
LYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR
VAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGDLSSDSRANADGYSLYDVEISI
IVQENAGSILCSIHLAEQSHEVESKVLIGETFFQSPWRLASILLGLLGCALCGVVMGMIIVFFK
SKGKIQAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF
TRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLSPNNGYWVLRLTTEHLYFT
FNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTLCQFEGLLRPYIQHAMYDEEKG
TPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 105

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAGGAAAAGAG
TTTGTGGGAACCTGGGTTATCGGCCCTCGTCATCTTCATATCCCTGATTGTCCTGGCAGTGTGCATTGGA
CTCACTGTTTATTATGTGAGATATAATCAAAAGAAGACCTACAATTACTATAGCACATTGTCAATTTACAAC
TGACAAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAACAATTTTACAGAAATGAGCCAGAGACTTGAAT
CAATGGTGAAAAATGCATTTTATAAATCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTC
AGTCAACAGAAGCATGGAGTGTGGCTCATATGCTGTTGATTGTAGATTTCACTCTACTGAGGATCCTGA
AACTGTAGATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG
ATCCTCACTCAGTTAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATGCTGCGGA
ACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAGAAGTAGAAGAGGGTGAATG
GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTTAATTAATGCCACATGGC
TTGTGAGTGTCTCACTGTTTTACAACATATAAGAACCCTGCCAGATGGACTGCTTCTTTGGAGTAACA
ATAAAACCTTCGAAAATGAAACGGGGTCTCCGGAGAATAATTGTCCATGAAAATACAAACACCCATCACA
TGACTATGATATTTCTCTTGAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTG
TCCCTGATGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAAT
GATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACTTGCAATGAACC
TCAAGCTTACAATGACGCCATAACTCCTAGAAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGCAT
GCCAGGGTGACTCTGGAGGACCCTGGTTAGTTTCAAGATGCTAGAGATATCTGGTACCTTGCTGGAATAGTG
AGCTGGGGAGATGAATGTGCGAAACCAACAAGCCTGGTGTATATACTAGAGTTACGGCCTTGCGGGACTG
GATTACTTCAAAAATGGTATCTAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTGT
GGTGTGGAGGCCATTTTATAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTCA
ATAAACTGTTTGCTTGATGCATGTATTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCA
GATCAACTCTGTCTCTGTGAGCAATAGTTGAACTTTATGTACATAGAGAAATAGATAATACAATATTAC
ATTACAGCCTGTATTCAATTTGTTCTCTAGAAGTTTGTGAGAATTTTGACTTGTGACATAAATTTGTAAT
GCATATATACAATTTGAAGCACTCCTTTCTTCAGTTCCTCAGCTCCTCTCATTTTCAAGCAATATCCATTT
TCAAGGTGCAGAACAAGGAGTGAAAGAAAATATAAGAAGAAAAAATCCCCTACATTTTATTGGCACAGAA
AAGTATTAGGTGTTTTCTTAGTGGAATATTAGAAATGATCATATTCAATATGAAAGGTCAAGCAAAGACA
GCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAACCTAAGTTAAGGAAGTCCAGAAAGAAGCCAAG
ATATATCCTTATTTTCATTTCCAAACAACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTGACCT
ATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATATTTATTTAACATTG
TTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 106

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTDKLY
AEFGREASNNFTEMSQRLESMVKNAFYKSPLEEFVKSQVIKFSQQKHGVLAHMLLICRFHSTED
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG
TEVEEGEWPWQASLOWDGSHRGATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKRGL
RRIIVHEKYKHPSHDYDISLAELSSFPYPTNAVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS
QNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSSGGLVSSDARDIWYLAG
IVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 107

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGGAAGAAGTTCCCTG
CCCCGATGAGCCCCCGCGTCCCGGACTATCCCCAGGCGGGCGTGGGGCACC GGCGCCAGC
GCCGACGATCGCTGCCGTTTTGCCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTCTCCCTT
ACGGGGCTCACAAATGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTACGCCCTCAA
TCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACCTAA
ATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTGACTTACTTTCCT
GTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCTTATCATTGTGGGGATGTTAGGATATTG
TGGAACGGTGAAAAGAAATCTGTGCTTCTTGCAATGTTGGAAGTTGCTTGTCAATTTCT
GTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTATGGTTCCAGTACAATGGTCA
GATATGGTCACTTTGAAAGCCAGGATGACAAATATGGATTACCTAGATATCGGTGGCTTACTCA
TGCTTGGAAATTTTTTTCAGAGAGAGTTAAGTGTGTGGAGTAGTATATTTCACTGACTGGTTGG
AAATGACAGAGATGGACTGGCCCCCAGATTCCGTGTGTGTAGAGAATCCCAGGATGTTCCAAA
CAGGCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTGTGGGAAGAAAATGTATTCCTT
TTTGAGAGGAACCAACAACACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAA
TCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCTGGG
ACAGACCAAATGATGCTCTTGAAGAATGACAACCTCTCAGCACCTGTCATGTCCCTCAGTAGAACT
GTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACT
TTGAGATGGAGGAGTTATAAAAAGAAATGTCACAGAAGAAAACCAAACTTGTTTTATTGGACT
TGTGAATTTTGTAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAA
TAACACCTAAGCATATACTATTCTATGCTTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTC
ACCACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC
TGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCGCA
TCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAA
CTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA
CTCAGCGATCTATTCTCTGATGCTAAATAAATTATATATCAGAAAACCTTCAATATTGGTGACT
ACCTAAATGTGATTTTGTCTGGTTACTAAATATCTTACCCTTAAAAGAGCAAGCTAACACAT
TGTCTTAAGCTGATCAGGGATTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCACTCGAT
TTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGCTCTGTATAGCATCATT
ATTTTGTAGCCTTTCTGTTAATAAAGCTTTACTATTCTGTCTGGGCTTATATTACACATATAAC
TGTTATTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTC
AGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTGAGA
AAGGACTTGTATGCTGTTTTTCTCCCAATGAAGACTCTTTTGGACACTAAACACTTTTTAAAAA
GCTTATCTTTGCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTTACAGAAAAA
TAGTGTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAACATGTGACAATTTAGAGATT
CTTTGTTTTATTTCACGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTACAA
GAGTATAGTATATTTATTTGAAATGGGAAAAGTGCAATTTTACTGTATTTTGTGATTTTGTATT
TTCTCAGAAATATGGAAGAAAATTTAAATGTGTCAATAATATTTCTAGAGAGTAA

FIGURE 108

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPVVHP
VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVT
LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGCSKQAHQ
EDLSDLYQEGCGKMYSLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDRREPQTDQM
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 109

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTTCTCTGATAAAGCCCTACCAGTGCT
GATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCTTAAAAAAAAAAGTGCTTGAAAGAGAAGGGGACAAAGGAACA
CCAGTATTAAGAGGATTTTCCAGTGTTCCTGGCAGTTGGTCCAGAAGGATGCCTCCATTCTGCTTCTCACCTG
CCTCTTCATCACAGGCACCTCCGTGTACCCGTGGCCCTAGATCCTTGTTCTGCTTACATCAGCCTGAATGAGC
CCTGGAGGAACACTGACCACCAAGTTGGATGAGTCTCAAGGTCTCCTCTATGTGACAACCATGTGAATGGGGAG
TGGTACCACCTTACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAACCCA
CGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAGGCGACGGCATTGTGCAACGCCAGGCTTGTGCCAGCT
TCAATGGGAACCTGCTGTCTCTGGAACACCACGGTGGAAAGTCAAGGCTTGCCCTGGAGGCTACTATGTGTATCGT
CTGACCAAGCCAGCGTCTGCTTCCACGTCTACTGTGGTCATTTTTATGACATCTGCGACGAGGACTGCCATGG
CAGCTGCTCAGATACCAGCGAGTGCACATGCGCTCCAGGAACTGTGCTAGGCCCTGACAGGCAGACATGCTTTG
ATGAAAATGAATGTGAGCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCTACCCTGT
GAGTGTGGGGTTGGCCGTGTGCTAAGAAGTGATGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAATAACAA
TGGTGGCTGCAGCCACTCTTGCCCTGGATCTGAGAAAGGCTACCAGTGTGAATGTCCCCGGGGCTGGTCTGT
CTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAAAATCAAATGCCATTGAAGTGAACATCCCCAGGGAG
CTGGTTGGTGGCTGGAGCTCTTCTGACCAACACCTCTGCCGAGGAGTGTCCAACGGGCACCCATGTCAACAT
CCTCTTCTCTCTCAAGACATGTGGTACAGTGGTGCATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGA
CAGGTCTACCCAAGCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTG
ACCTGCGAGTTTCCACGCCTGTACACATTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCCACTGCAAAT
CATGAGCCGAAATCATGGGATCTTCCCATTCACTCTGGAGATCTTCAAGGACAATGAGTTTGAAGAGCCTTACC
GGGAAGCTCTGCCACCCCTCAAGCTTCGTGACTCCCTCTACTTTGGCATTGAGCCCGTGGTGCACGTGAGCGGC
TTGGAAAGCTTGGTGGAGAGCTGCTTTGCCACCCCACTCCAAGATCGACGAGGTCTGAAATACTACCTCAT
CCGGGATGGCTGTGTTTCAGATGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGG
TCCCTGTCTTCAAGTTTGTGGGCAAAGACCACAAGGAAGTGTTCCTGCACTGCCGGGTCTTGTCTGTGGAGTG
TTGGACGAGCGTTCCCGCTGTGCCAGGGTTGCCACCGGCAATGCGTCTGGGGCAGGAGGAGAGGACTCAGC
CGGTCTACAGGGCCAGACGCTAACAGGCGGCCGATCCGCATCGACTGGGAGGACTAGTTCGTAGCCATACCTC
GAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTCCCCCACCGCCCTCTAAGAACATCTGCCAACAGC
TGGGTTACAGACTTCACACTGTGAGTTCAGACTCCAGCACCAACTCACTCTGATTCTGGTCCATTCACTGGGCA
CAGGTCACAGCACTGTGAACAATGTGGCCTGGGTGGGGTTTCATCTTTCTAGGGTTGAAACTAAACTGTCCA
CCCAGAAAGACACTCACCCCATTTCCCTCATTTCTTCTACACTTAAATACCTCGTGTATGGTGAATCAGAC
CACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAAACCCTAGAAAAATTAACAGTTACTGAAATTATGA
CTTAAATACCCAAATGACTCCTTAAATATGTAAATTATAGTTATACCTTGAAATTTCAATTCAAATGCAGACTAA
TTATAGGGAATTTGGAAGTGTATCAATAAACAGTATATAATTTT

FIGURE 110

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHLDESQGPPLCDNHVNGEWYHFTGMAGDAMP
TFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPGGYVYRLTKPSVCFHV
YCGHFYDIDCEDCHGSCSDTSECTCAPGTVLGPDROTCDENECEQNNGGCSEICVNLKNSYRCECGVGRV
LRSDGKTCEDVEGCHNNNGGCSHSLGSEKGYQCECPRLVLSNHTCQVPVLCKSNAIEVNIPRELVG
LELFLTNTSCRGVSNNGTHVNLFLSLKTCGTVDVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT
CEFPRLYTISEGYVFNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEEPYREALPTLKLRLDSLYFGIEPVVHV
SGLESLEVSCFATPTSKIDEVLKYILRDGCVSDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV
LVCGVLDERSRCAQGCHRRMRGAGGEDSAGLQGQTLTGGPRIIDWED

Important features of the protein:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

Tyrosine kinase phosphorylation sites.

amino acids 411-418, 443-451

N-myristoylation sites.

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,
522-528, 531-537

Aspartic acid and asparagine hydroxylation site.

amino acids 197-209

ZP domain proteins.

amino acids 431-457

Calcium-binding EGF-like proteins.

amino acids 191-212, 232-253

FIGURE 111

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGG
GCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCT
CCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT
TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCC
ATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGT
GGTTGTCTCATCAAGGTGATTCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGA
GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC
CCCGAAGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCCACTGCAGGTGCTGGACTCGGCCAC
AGGGAACCTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGG
GCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGATGTTGTTGAAATCACAGAAACAGCCAG
GAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCCTG
TGGGAAGAGCCTGAAGACCCCCGTGTGGTGGGTGGGGAGGAGCCTCTGTGGATTCTTGGCCTTGGCAGG
TCAGCATCCAGTACGACAAACAGCAGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCA
GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGCAG
CTTCCCATCCCTGGCTGTGGCCAAGATCATCATATTGAATTCAACCCCATGTACCCCAAAGACAATGACA
TCGCCCTCATGAAGCTGCAGTTCCTCACTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTT
GATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAA
GATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTATTGACAGCACACGGTGCAATGCAGACGATGCGT
ACCAGGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGAAGGGGGTGTGGACACCTGCCAGGGT
GACAGTGGTGGGCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGG
CTGCGGGGGCCCCGAGCACCCAGGAGTATACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT
GGAAGGCTGAGCTGTTAATGCTGCTGCCCCTTTGAGTGCTGGGAGCGCTTCCTTCCCTGCCCTGCCACCT
GGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCAT
TTCTTGGAGCAGCAAAGGGCCTCAATTCTGTAAAGAGACCCTCGCAGCCAGAGCGCCAGAGGAAGTCA
GCAGCCCTAGCTCGGCCACACTTGGTGCTCCCAGCATCCAGGGAGAGACACAGCCCACTGAACAAGGTCT
CAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAAGCC
CAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAA
GCCTACTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT
ACTGTTGTCATTGTTATTACAGCTATGGCCACTATTATTAAGAGCTGTGTAACATCTCTGGCAAAAAAA
AAAA

FIGURE 112

MLQDPDSQPLNSLDVKPLRKPRIPMETFRKVGIPITIIALLSLASIIIVVLIKVIIDKYYFLCG
QPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN
FTEALAEACRQMGSRAVEIGPDQDLDVVEITENSQELMRNSSGPCLSGSLVSLHCLACGKSL
KTPRVVGEEASVDSWPWQVSIQYDKQHVCSSILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKL
GSFPSLAVAKIIIIIEFNMPYKDNIDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWG
FTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCQGDSSGGPLMYQS
DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 113

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGATTA
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTTCAGCAACTAAAAAGCCACAGGAGT
TGAACCTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATTAAATC
TGTTTTTTGTTCTCTTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGTCACTGTGGCTCT
GGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGTCCCCCTGAAG
CCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAACTGTCTCACGTCT
GGAGGCACTGACTCGGGCAGTGACAGGTAGCTGAGCCTCTTGCTAGCTGCGGCTTTCAAGGTGGGC
CTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATTTTCATAGGCGATGGCTCCCCTGCCC
AGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGGGCCGTGGACACCTGCTCA
GAAGCAGTGGGTGAGACATCACGCTGCCCCGCCATCTAACCTTTTCATGTCCTGCACATCACCTG
ATCCATGGGCTAATCTGAACTCTGTCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC
CAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGACTTGCAATTCTCCTGGAACATGAGG
GAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACTTGTGCCAAATTATGGGTCAGAAAAGATG
GAGGTGTTGGGTTATCACAAGGCATCGAGTCTCCTGCATTAGTGACATGTGGGGGAAGGGCTG
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGAT
CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAA
TCTGCGATCACCAGCCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCC
CTCCTTCCCTCTGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG
GGCTAATGGCTCAGTGTGGCCAGGAGGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCT
GTGCGAACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGG
CTCAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCAAGACCAAAGGAGCTAGAGCTTGGTT
CAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAATCCA
AACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACAT
TTTGGGAGGCCGAGCGGGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGG
TGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATC
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACA
GGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAAGAATTA
TGTTTATTTGTAA

FIGURE 114

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC
WPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

Signal peptide:

amino acids 1-15

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC
WPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

FIGURE 115

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA
AGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAA
ATATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCTAATTGTCCT
GTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT
TCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAGAACTGAAATA
TTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAACGGATACACTGG
CATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGATTAAAGTGATTCCTGAATTTT
CTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTTTCTTTGAACAGTCAGTG
ATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATTCTGGA
GATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAG
ACTTTGAGGAGGAGGAGAAGATCTTCACTTTCTGCCAACGAAAAAAGGGATTGAACAAAAT
GAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGA
AGAACTTCCAATAAATGACTATACTGAAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAG
GTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTA
GGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTG
TAACTGGTGGGTGGCCCGCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAATGCTTAAAC
TGCTGGCAACATATAATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCCT
GGTAGCCAGCTCTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACA
TTATCACCAAAAAAAAAAAAAAAAAAAAA

FIGURE 116

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPPKKAYDME
HTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKTQIKVIP
EFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNKILEICDNVTMYWINPTLISVSE
LQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLD
ERGYCCIIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV

Important features of the protein:

Signal peptide:

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-
242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 117

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGCAGGCGGCA
GGCGGGGCGGCCAGGATCATGTCCACCACCACATGCCAAGTGGTGGCGTTCTCCTGTCCATCCTGGGGCT
GGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCAGGACCTGTACGACAACCCCGTCACCT
CCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCC
TATTTACCATCCTGGGACTTCCAGCCATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCT
GGGTGCCATTGGCCTCCTGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG
CCAAAGCCAACATGACACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTG
TCTGTGTTTCCCAACATGCTGGTGACTAATTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTGG
GATGGTGCAGACTGTTTACAGACAGGTACACATTTGGTGCGGCTCTGTTCTGGGCTGGGTGCTGGAGGCC
TCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCCTGGCACCAGAAGAAACCACTACAAA
GCCGTTTCTTATCATGCCTCAGGCCACAGTGTTCCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTT
TGGGTCCAACACCAAAAACAAGAAGATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATC
CTTCCAAGCAGACTATGTGTAAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCA
CCCAAAAACAAGGAGATCCCATCTAGATTCTTCTGCTTTTGAATCAGCTGGAAGTTAGAAAAGCCT
CGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCACCATAAAACA
GCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTTCTTTTTTAAATATAACT
TTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAGACTCCCCCTC
TTCTCCTAGTCAATAAACCCATTGATGATCTATTTCCAGCTTATCCCAAGAAAACTTTTGAAAGGAAA
GAGTAGACCCAAAGATGTTATTTCTGCTGTTTGAATTTGTCTCCCCACCCCAACTTGGCTAGTAATAA
ACACTTACTGAAGAAGAAGCAATAAGAGAAAAGATATTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTT
ACACTGTGATCTTAAAAGTTACCAAACCAAAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTGCTG
TTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAGTCCTCTTTCTGT
CGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAATTTAAGTCCTAAATATAGTTAA
AATAAATAATGTTTTAGTAAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAGAAG
GAAATGAAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTC
ATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGT
TCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCA
TGGTGGCATACACCTGTAGTCCCAGCATTCGGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGT
TGGGGCTGCAGTGAGCCATGATCACACCCTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA
AATAAAAAATAAATAATGGAACACAGCAAGTCTAGGAAGTAGGTTAAACTAATTCTTTAA

FIGURE 118

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTECRP
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFIVSGL
CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYPSKHDY
V

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 119

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCGGAGTCC
AGCTGGCTAAAACATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTG
GTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGAGTGTGGCCTTCATT
GAAACAACATCGTGGTTTTTGAACCTTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA
CATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTTTCTCCGGACCTACAGGCAGCCAGAG
GACTGATGTGTGCTGCTTCCGTGATGTCTTCTTGGCTTTCATGATGGCCATCCTTGGCATGAAATGC
ACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCAT
CATCACGGGCATGGTGGTGCTCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATA
ACTCAATAGTGAATGTTGCCCAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCA
CTGGTGCTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTGTGCAACGAAAAGAGCAGTAGCTA
CAGATACTCGATACCTTCCCATCGCACAAACCAAAAAAGTTATCACACCGGAAAGAGTCACCGAGCG
TCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTAACTTTACTATAAAGCCATGCAAATG
ACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAGAACTTTGATTTACTGTTCTTAACTGCCT
AATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTACGAGAATGAGATA
TTAAACCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAAGCATCTA
CTCTTTTATCATTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAATTTCTCC
ACGACATAGCATTATGTACATAGATGAGTGTAACTTTATATCTCACATAGAGACATGCTTATATGGT
TTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAA
ATCATGGATAGGGTTGAAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCA
TTTATAATGAAGATTAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATAT
GCTGTTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTTT
CTTGTGTATTAAATTAACATTTTTTAAACGCAGATATTTGTCAAGGGGCTTTGCATTCAAACGCTT
TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAGTGATGTTTTAGGAAAGTG
AAAATATTTTTGTTTTGTATTTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGAT
ATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAAGAGCAGAAAAATA
TGTCTTGTTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTCACCT
GCTCCTATGTGGGTACCTGAGTCAAAATGTCAATTTTTGTCTGTGAAAAATAAATTTCTTCTTGTA
CCATTTCTGTTTAGTTTTACTAAATCTGTAAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAA
ACTGACAATCCAATTTGAAAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTT
TATACATTTATATTAATAAATTTGTACATTTTTCTAATT

FIGURE 120

MATHALEIAGLFLGGVGMVGTVAVTVMPOWRVSAFIENNIVVFENFWGLWMNCVRQANIRMQCK
IYDSLLALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITG
MVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCNEKSSSY
RYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 121

GGAGAGAGGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGGGAG
CCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCAGCC
GGGAGCCATGCGACCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTGCTGCTCC
TGCTGCTGCAGCTGCCCGCGCGTGCAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAG
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC
TGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTGGGATG
GATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCTGGACACCCAACTAC
AAGCAGTGTTTCATGGAGTTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGACATT
TACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTTCAGTGGCTCACTTCGGCTAAAATGCA
GAAATGCATGCTGTGAGCGTTGGTATTTACATTCAATGGAGCTGAATGTTTCAGGACCTCTTCCC
ATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCG
CACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG
TTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATC
ATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTGCTACCTCTTTTTTTATTATGCC
TTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAG
CTAAATATGTTTACAGACCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTG
CTTCAATCAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTCTTCATAGTCACATT
CTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTA
AAAAATATAAAAGCTACCAATCTTTGTACAATTGTAAATGTTAAGAATTTTTTTTATATCTGT
TAAATAAAAATTATTTCCAACA

FIGURE 122

MRPQGPAASPQRLRGLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAAGVPGR
DGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGGLPIEAIYLDQGSPPEMNSTINIHRTS
SVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 123

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTGAA
CTGGGTGCTCATCACGGGAACGTCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA
ATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTTTTTTTA
ACCGCCCCCTCCCCACCCCCAAAAAACTGTAAAGATGCAAAAACGTAATATCCATGAAGATCC
TATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTTGTTCTTGGAG
TGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAGGGGTCCAATTTT
TCTTCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCGAGCTGACAGGGGCTGTGCACTG
GCCCTAAGCCAAAGCAAAGACCTAAGGACGACCTTTGAACAATACAAAGGATGGGTTTCAATG
TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCACTGTCTTACTGACAATG
CTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAAGGCAAAATGGTATATTGTGA
ATCTCAGAAATTACAGGAGATACCCCTCAAGTATATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCT
ATAACAGCCTTCAAAAACCTTAAGTATAATCAATTTAAAGGGCTCAACCAGCTCACCTGGCTATAC
CTTGACCATAACCATATCAGCAATATTGACGAAAATGCTTTTAAATGGAATACGAGACTCAAAGA
GCTGATTCTTAGTTCCAATAGAAATCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAAT
TACGGAACCTGGATCTGTCTATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTG
CGGAAGCTGCTGAGTTTACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCA
AGACTGCCGCAACCTGGAACCTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATG
TCTTTGCTGGCATGATCAGACTCAAAGAACCTCACCTGGAGCACAATCAATTTTCCAAGCTCAAC
CTGGCCCTTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAATAAAATCAGTGT
CATAGGACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGA
TCGAAGCTTTTCAAGTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGAT
TCCAACAAGCTCACATTTATTTGGTCAAGAGATTTTGATTCTTGGATATCCCTCAATGACATCAG
TCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAAGCTGGCTGAAAAGTT
TTAAAGGTCTAAGGGAGAATACAATATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTG
ATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAG
GGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAAACCCCTT
TGCCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGCTGACGCCGAGCACATCTCT
TTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCGTGCTCGTCATCCTGCTGGTTAT
CTACGTGTGATGGAAGCGGTACCCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAA
GGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCAGCACCCAGGAATTTTATGTA
GATTATAAAACCCACCAACACGGAGACAGCGAGATGCTGCTGAATGGGACGGGACCCCTGCACCTA
TAACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATTTGTGATAAAAAGAGCTCTTAAAGCT
GGGAAATAAGTGGTGTCTTATTGAACTCTGGTGACTATCAAGGGAACGCGATGCCCCCTCCCC
TTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCTTGTCCGTTTTAGTGCATTCAATAACT
GGTCATTTTCTCTCATAATAATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTT
GAACTCCGGTTTAAATATAATACCTATTGTATAAGACCCTTTACTGATTCCATTAATGTGCGATTT
GTTTTAAGATAAACTTCTTTTCATAGGTAAAAA

FIGURE 124

MGFNVIRLLSGSAVALVIAPTPLLTLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAGCLG
LSLRYSNLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYFLNNTFR
PVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIFQDCRNLELLDLGYNRIRS
LARNVFAGMIRLKEHLHLEHNQFSKLNALFPRLVSLQNLQWNKISVIGQTMSTWSSQLRDL
SGNEIEAFSGPSVFCVFNLRNLDSNKLTFIGQEILDSWISLNDISLAGNIWECSRNICSLVN
WLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRPKHE
SKPPLPPTVGATEPGPETDADAHEHISFHKIIAGSVALFLSVLVILLVIYVSWKRYPASMKQLQQR
SLMRRHRKKRQSLKQMPSTQEFYVDYKPTNTETSEMLLNGTGPCTYNKSGSRECEV

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 125

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCGCTG
ACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGCCGAGCT
AGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAGCTCTTGCTC
GGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACAGCCCTAGGGATC
ATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTTACAGACACGTAGT
GTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTTGGCAAAAGTGAAG
ATGAGCATTATCCCCCTTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCCAGTTT
TTAGCCAATCCAATGACCTAGTGAAGGTTGAGATGCAAATGGAAGGAAAAAGGAACTGGAAGG
AAAACCATTGCGATTTTCGTGGTGTACATCATGCATTTGCAAAAATCTTAGCTGAAGGAGGAATAC
GAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTA
ACCACCTTATGATACAGTGAAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGAC
TCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA
TCAAAGCAGAATAATGAATCAACCACGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCG
ACTGACTGCTTGATTCAAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACC
ATCTTGGCTGAGAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAATCAGAGAGA
TGAGTGGAGTCAGTCCATTTTAA

FIGURE 126

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGARES
APYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVKSEDEHYPLWKS
VIGGMMAGVIGQFLANPTDLVKVQMMEGKRLKLGKPLRFRGVHHAFKILAEGGIRGLWAGWVP
NIQRAALVNMGDLTTYDTPVKHYLVNTPLEDNIMTHGLSSLCSGLVASILGTPADVIKSRIMNQP
RDKQGRGLLYKSSTDCLIQAVQGEFGMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 127

CGCGGATCGGACCCAAGCAGGTCGGCGGGCGGCGCAGGAGAGCGGCCGGGCGTCAGCTCCTCGAC
CCCCGTGTCGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCCCATGCCAGGCCCCGGCATGG
AGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCTCGGGGGGCATCGCGCGGGCCGTGGCC
CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAACATCGAGGA
GCTGGCTGCTGAATGTAAGAGTGACAGGCTACCCCGGGACTTTGATCCCCCTACAGATGTGACCTAT
CAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATC
TGCATCAACAATGCTGGCTTGGCCCCGGCCTGACACCCTGCTCTCAGGCAGCACCAGTGGTTGGAA
GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAGTCCATGA
AGGAGCGGAATGTGGACGATGGGCACATCATTAAATCAATAGCATGTCTGGCCACCGAGTGTTA
CCCCGTGCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGGACT
GAGGCAAGAGCTTCGGGAGGGCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGGTGTGGTGG
AGACACAATTGCGCTTCAAACCTCCACGACAAGGACCCTGAGAAGGCAGCTGCCACCTATGAGCAA
ATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCCTCAGCACCCCCGCACA
CATCCAGATTGGAGACATCCAGATGAGGCCCCACGGAGCAGGTGACCTAGTGACTGTGGGAGCTCC
TCCTTCCCTCCCCACCCTTCATGGCTTGCCTCCTGCCTCTGGATTTTAGGTGTTGATTTCTGGAT
CACGGGATACCACTTCCTGTCCACACCCCGACCAGGGGCTAGAAAATTTGTTTGAGATTTTATA
TCATCTTGTCAAATGCTTCAGTTGTAATGTGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCC
TAATTGTTTTACTTGTTAACTTGTTCTTGTGCCCCCTGGGCACCTTGGCCTTTGTCTGCTCTCAGTG
TCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCCCCATCTTCTGCACCTCAACGTCTG
TGGCTCAGGGCTGGGGTGGCAGAGGGAGGCCTTACCTTATATCTGTGTTGTTATCCAGGGCTCC
AGACTTCCTCCTCTGCCTGCCCCACTGCACCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCC
AGCCCAGTCTTGGCTTCTTGTCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAG
CAGAACACCAGGGCCTGGCCCAGTGGATTTTCATGGTGATCATTAAAAAAGAAAAATCGCAACCAA
AAAAAAAAAA

FIGURE 128

MARPGMERWRDRLALVTGASGGIGAARALVQQGLKVVGCAITVGNIEELAAECKSAGYPGTLI
PYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPDITLLSGSTSGWKDMFNVNVLALSICTR
EAYQSMKERNVDDGHIININMSGHRVLPISVTHFYATKYAVTALTEGLRQELREAQTHIRATC
ISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

Important features of the protein:

Signal peptide:

amino acids 1-17

N-myristoylation sites.

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,
199-205

Short-chain alcohol dehydrogenase.

amino acids 30-42, 104-114

FIGURE 129

AACTTCTACATGGGCCTCCTGCTGCTGGTGTCTTCCTCAGCCTCCTGCCGGTGGCCTACACCAT
CATGTCCCTCCCACCTCCTTTGACTGCGGGCCGTTCAAGTGCAGAGTCTCAGTTGCCCCGGAGC
ACCTCCCCCTCCCAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATTCCAGTTCTGGTTTCATGC
CAGCCTGTAAAAGGCCATGGAACCTTGGGTGAATCACCGATGCCATTTAAGAGGGTTTTCTGCCA
GGATGGAAATGTTAGGTGCTTCTGTGTCTGCCCTGTTCAATTCAGTAGCCACCAGCCACCTGTGG
CCGTTGAGTGCTTGAAATTGAGGAACTGAGAAAATTAATTTCTCATGTATTTTTCTCATTTATTTA
TTAATTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGGATACATGTATACAA
TATATAATGATCAAATCAGGGTAACTGGGATATCCATCACATCAAACATTTATTTTTTATTCTTT
TTAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC
CTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAAGTAGCTGGGACTACAGGCAT
GCACCACAATGCCCAACTAATTTTTGTATTTTTAGTAGAGACGGGGTTTTGCCATGTTGCCCAGG
CTGGCCTTGAACFCCTGGCCTCAAACAATCCACTTGCCCTCGGCCTCCCAAAGTGTATGATTACA
GGCGTGAGCCACCGTGCTGGCCTAAACATTTATCTTTTCTTTGTGTTGGGAACCTTTGAAATTAT
ACAATGAATTATTGTAACTGTCATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT
ATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCC
AACCTCTGATCACCTCATTCTACTCTCTACCTCCATGAGATCCACTTTTTTAGCTCCCACATGTG
AGTAAGAAAATGCAATATTTGTCTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTCCTG
TTCCATCCATGTTGCTGCAAATGACAGGATTTCTGTTCTTAATTTCAATTAAAATAACCACACATG
GCAAAAA

FIGURE 130

MGLLLLVLFLSLLPVAYTIMSLPPSFDGPFRCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQPV
KGGHTLGESEMPFVKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

FIGURE 131

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAGCCTGGAGC
ATCTTCCTCATCGGGACTAAAATTGGGCTGTTCCTTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG
TCCATCTGTGTGCTGCGTGCATGCGGGTTTCATTTACTGTAATGATCGCTTTCTGACATCCATTCCAACAG
GAATACCAGAGGATGCTACAACCTCTACCTTCAGAACAACCAAATAAATAATGCTGGGATTCCCTCAGAT
TTGAAAAACTTGCTGAAAGTAGAAAGAATATACCTATACCACAACAGTTTAGATGAATTTCCACCAACCT
CCCAAAGTATGTAAGAGGTTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAA
AAATTCCCTATCTGGAAGAATTACATTTAGATGACAACCTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCA
TTCCGAGACAGCAACTATCTCGACTGCTTTTCCTGTCCCGTAATCACCTTAGCACAATTCCCTGGGGTTT
GCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTATCACCATCTCTTCAAG
GTCTCACTAGTCTAAACGCGCTGGTTCTAGATGGAACCTGTTGAACAATCATGGTTTAGGTGACAAAGTT
TTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCGGAATTCCTGACTGCTGCACCAGTAAACCT
TCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATAACCACATCAATCGGGTGCCCCCAATGCTTTTT
CTTATCTAAGGCAGCTCTATCGACTGGATATGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTT
GATGATTTGGACAATATAACACAACCTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATG
GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAA
AGGTTTCGTGGGATGGCTATTAAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAAGC
ACCATTCAAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCCAAGGACAGTGGCCAGCTCCAGTGAC
CAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAGGGAGTCCCTCAAGAAAAA
CAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTATCTCTTGGAACCTTGCTCTACCTATG
ACTGCTTTGAGACTCAGCTGGCTTAACTGGGCCATAGCCCGGCATTGGATCTATAACAGAAACAATTGT
AACAGGGGAACGCAGTGAGTACTTGGTCACAGCCCTGGAGCCTGATTACCCTATAAAGTATGCATGGTTC
CCATGGAAACCAGCAACCTCTACCTATTTGATGAAACTCCTGTTTGTATTGAGACTGAAACTGCACCCCTT
CGAATGTACAACCCCTACAACCACCCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTTACC
TTTGGCTGCCATCATTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTTGGTATG
TTCATAGGAATGGATCGCTCTTCTCAAGGAAGTGTGCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT
GCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAAACTTCTTTTCAGATGTTACCAAT
AAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAAACACACCATATTTCTCCTAATGGAATGAATCTGT
ACAAAAACAATCACAGTGAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACTCAGATCAC
TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTTGGGTTTTTTTAAACCTAAGGGAGGTGATG
GT

FIGURE 132

MISAAWSIFLIGTKIGLEFLQVAPLSVMAKSCPSVCRCDAGFIYCNDRFLTSIPTGIPEDATTLYL
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRITITYDSLSKIPYL
EELHLLDDNSVSAVSIEEGAFRDSNYLRLFLSLRNHLSTIPWGLPRTIEELRLDDNRISTISSPSL
QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKLYLQDNHIN
RVPPNAFSYLRLQYRLDMSNNNLSNLPQGIFDDLDNITQLILRNPNWYCGCKMKWVRDWLQSLPV
KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQGQWPAPVTKQPD
IKNPKLTKDQQTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRLSWLKLGHSPAFGSITET
IVTGERSEYLVTALEPDSPYKVCMPMETSNNLYLFDETPVCIETETAPLRMYNPPTTLNREQEKE
PYKNPNLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNS
ILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLKNNHSESSNRSYRDSGIPDSHSHS

Important features of the protein:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 531-552

N-glycosylation sites.

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

Tyrosine kinase phosphorylation site.

amino acids 515-522

N-myristoylation sites.

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,
640-645

Amidation site.

amino acids 567-570

Leucine zipper pattern.

amino acids 159-180

Phospholipase A2 aspartic acid active site.

amino acids 34-44

FIGURE 133

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCAGGCCACCCAGGCTTCTTGGCA
GCCCTGCCGGGCCACTTGTCTTCATGCTCTGCCAGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG
TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGAGCAGAG
GCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACCGTGTGGT
CCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCTGATCCTGTCT
GCGCTGGAGAGAGCCACCGTCTTCCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT
GGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCGGGAGAAGTGGGCCCAGGAGCCCTGC
TGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC
CTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCAGCTGACCCTCCAGCCCGG
GTTTTGGAAGCTCCCACATGCCTGGATCCACACTGATGCCTCCTTGGTGTACCCACGTTCCGGG
CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGTGCAGCTGCTGGGAACCGGACG
GACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCCGGCTGCTC
AGGCTACTGCCTGTCCCACCAACTGCTCTTCTTCCTCTGGGCCAGAATGAGGGGATGCACACAGG
GACCACTCCAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC
AGAGCTGAGGCCATCGGATACGCCTACCCTACCCGGGACATCTTCATGGAACATCATGTTCTG
TGAATGGGCGGCTTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA
AACAGCAGGAAGGATGCTTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA
TATCAGCAGCATTTTTTCGAGGAGAGTGAAGAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGT
TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAGC
AATTCTCTTGCTCATCCTCCCAGTAGCTGGGACTACAGGAGCGTGCCACCATACCTGGCTAAT
TTTTATATTTTTTAGTAGAGACAGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGAT
CTCAAGAGATCCGCCACCTCAGGCTCCCAAAGTGTGGGATTATAGGTGTGAGCCACCGTGTCTG
GCTGAAAAGCACTTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTC
ATGGGGGCTCTCTCCCTAGATGGCTGCTCCTCCACAACACAGCCACAGCAGTGGCAGCCCTGG
GTGGCTTCTATACATCCTGGCAGAATACCCCCAGCAAACAGAGAGCCACACCCATCCACACCG
CCACCACCAAGCAGCCGCTGAGACGGACGGTTCATGCCAGCTGCCTGGAGGAGGAACAGACCCC
TTTAGTCCTCATCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG
ATAAGCAAAGCCACCCGACACCCAATCTTGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG
GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAA

FIGURE 134

MSARGRWEGGRRACRGSGLARAQGAERTVSSEQRPMASLGLLLLLLTALPPLWSSSLPGLD
TAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPLSLRV
GMLGEKLEAAIQRS LHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE
RSDVCLVQLLGTGTDSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGFLQOSQD
YINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILS WQKQEGCFG
EPDAEDEELSKAIQYQQHFSSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFKQFSCLILP
SSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPPTSGSQSVGL

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 39-56

Tyrosine kinase phosphorylation sites.

amino acids 149-156, 274-282

N-myristoylation sites.

amino acids 10-16, 20-26, 63-69, 208-214

Amidation site.

amino acids 10-14

Glycoprotein hormones beta chain signature 1.

amino acids 230-237

FIGURE 135

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTG
CTGCTGCTATCGGGGATGTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGG
GAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAAGTTGTTCCAGGGGTGAAGC
CTCAGGACTGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAG
ACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGAAGTTGTATCTCC
AGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCAAGATATG
TGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATGAAATCTTCAGGT
CCACCTTCTTACTTTATTAAAGGGAATCGTGGGGCTGGACAGACTTTCTAATGAACCCAATGGT
TATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAGTGGTCAACACAAGTGATC
CTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATCCAACCATGAGTTGCCTGAT
GTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAATCATCTGGCAAATCTAGCAGCGGCAGCAG
TAAACAGGCAAAAGTGGGGCTGGCAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTTCAC
AAACACGGCAACACTGGGTGGCATCCAAGTCTTGAAAACCGTGTGAAGCAACTACTATAAACTT
GAGTCATCCCGACGTTGATCTCTTACAACGTGTATGTT
AACTTTTGTAGCACATGTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGTAT
GAGGTCAATATTGATGTCAGTGAATTAATTACAGTGTCCTATAGAAAATGCCATTAATAAATTAT
ATGAACACTATACATTTATGTATATTAATTAAACATCTTAATCCAGAAATCAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 136

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGSGVGIGDRFKIEGRAVVPGVKPDWISAA
RVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVS PAYRFDPVRVDITSKGMRARYVNYIKTSE
VVR LPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLPLLI FVLLPKVNTSDPDMRREME
QSMNMLNSNHELDPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR

Important features of the protein:

Signal sequence:

amino acids 1-23

Transmembrane domain:

amino acids 161-182

N-glycosylation site.

amino acids 184-187

Glycosaminoglycan attachment sites.

amino acids 37-40, 236-239

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 151-154

N-myristoylation sites.

amino acids 33-38, 36-41, 38-44, 229-234

Amidation site.

amino acids 238-241

ATP/GTP-binding site motif A (P-loop).

amino acids 229-236

FIGURE 137

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTCTCCCCAGTTCCCCTGTGGGTCTGAGGGGA
CCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAAACAA
GTTTTGACATTTCCCGTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTTCCAGGC
CTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACGACCTGTGC
CACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTTTCACGGGAGGCTTGGCAGT
TTTTCTTACTCCTGTGGTCTCCAGATTTCAAGCCTAAGATGAAAGCCTCTAGTCTTGCCTTCAGC
CTTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAGACACTCAATTTGGG
AAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAGTG
TGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAAGACACA
AAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTGCTAAGACTCTATCTGGACAGGGTATTTAA
AAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTCGCCAATTCCTTTCTTA
CCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACATGCCATTGTGGGGAGGAAGCAATG
AAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGC
TTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTG
CTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAA
ACCACCATCTCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTG
CTTCCTTGCAATGATTGCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTT
TGTAATATCTTTCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTTGCTATTTA
ATGTATTTATTTTTTTTACTTGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTG
ACTAGAGCAGGTGATGTATTTTTATACAGTAAAAAAAACCTTGTAATCTAGAAGAGTGG
CTAGGGGGGTATTCAATTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGAT
ATTTGAAATGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATTGCAC
ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAG
CCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTCTTTGCATACCAAAAAAAA
AAAAAAAAAA

FIGURE 138

MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEPGWGQNGATT CATNSHSDSEL RPEIF
SSREAWQFFLLWSPDFRPKM KASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG
FSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKIS
SLANSFLT IKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEET
E

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 139

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCCGCATCCAGCC
TAGCGTGTCCACGATGCGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCGAGGTGC
TAGGGATCGCGGTCTTCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCCCTTGCCAGAGCGGAA
CACGGAGCGGAGCCCCAGCGCCCGAACCTCGGCTGGAGCCAGTTCTAACTGGACCACGCTGCC
ACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAGATGATTTTGTGTTG
GGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTACCTTGTGAAAAAGGAGCATCTCACAGT
TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAATCAAGGCATTGATGACGGGGAG
CCTTCTGGCTTTGTGACGTCATCAGGAACCTCAATTCTCCTGCACTGCTGGAAGACAGTGTGA
TAAGACAAGCAAAGCAGCTGGAAGAAAGATAGTCTTTTATGGAGATGAAACCTGGGTAAATTA
TTCCCAAAGCATTTTGTGGAATATGATGGAACACCTCATTTCGTGTCAGATTACACAGAGGT
GGATAATAATGTCACGAGGCATTTGGATAAAGTATTAAGAAAGAGGAGATTGGGACATATTAATCC
TCCACTACCTGGGGCTGGACCACATTGGCCACATTTAGGGCCCAACAGCCCCCTGATTGGGCAG
AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTGAAGGAGAGAGA
GACGCTTTTACCCAAATTTGCTGGTTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAATCAGC
GGGCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCTGCGTTTGAAGGAAA
CCCGGTGATATCCGACATCCAAAGCACGTCCAATAGACGGATGTGGCTGCGACACTGGCGATAGC
ACTTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTCCTATTCCAGTTGTGGAAGGAAGAC
CAATGAGAGAGCAGTTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAG
AATGTCCGTCATATGAAAAGATCCTGGGTTTGAACAGTTTAAATGTCAGAAAGATTGCATGG
GAACGTGATCAGACTGTACTTGGAGGAAAAGCATTCAGAAGTCTATTCAACCTGGGCTCCAAGG
TTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCAG
TTCTCACCTGCTCCTGCTCAGCGTCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCA
CTGTCTATCTCCTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTCGGCCGTTACGT
CATTGTGTGCACCTCAGCTGAAAGTTTCGTGCTACTTCTGTGGCCTCTCGTGGCTGGCGGCAGGCT
GCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGTGGCAGTGCCTGGAC
AGGGGGCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCCCTCTGGGTGTCCGACACAGGTG
TTCACATCTGTGCTGTCAGGTCAGATGCCTCAGTTCTTGGAAAGCTAGGTTCCCTGCGACTGTTAC
CAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGTGAA
TCGGACAGCCTCCAGCAGAGGTGTGGGAGCTGCAGCTGAGGGAAGAAGAGACAATCGGCCTGGA
CACTCAGGAGGGTCAAAGGAGACTTGGTCGCCACCACTCATCTGCCACCCCAAGATGCATCCT
GCCTCATCAGGTCCAGATTTCTTTCCAAGCGGACGTTTTCTGTTGGAATTCTTAGTCTTTGGCC
TCGGACACCTTCATTTCGTTAGCTGGGGAGTGGTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCAC
ACTCAGATCCACAGAGCCCAGGATCAAGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCC
ACCCCAACCCTGCACAGCCCTCATCCCCTCTTGGCTTGAGCCGTCAGAGGCCCTGTGCTGAGTGT
CTGACCGAGACACTCACAGCTTTGTCATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTG
CCACGCTGACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTCTGCTATTGAATTAGTACCTAG
CTGCACACAGTATGTAGTTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA

FIGURE 140

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGAEPPAPEPSAGASSNWTTLPPPLF
SKVVIVLIDALRDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF
VDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPKHFEYDGTTSFFVSDYTEVDNNV
TRHLDKVLKRGDWDILILHYLGLDHHIGHISGPN SPLIGQKLSEMDSVLMKIHTSLQSKERETPLP
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

Important features of the protein:

Signal peptide:

amino acids 1-34

Transmembrane domain:

amino acids 58-76

N-glycosylation sites.

amino acids 56-60, 194-198

N-myristoylation sites.

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,
275-281, 278-284

Amidation site.

amino acids 154-158

Cell attachment sequence.

amino acids 205-208

FIGURE 141

GGCACGAGGCAAGCCTTCCAGGTTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTACA
GAAAGTTACTAGTGCCTAAAGCTGGCGCTGGCACTGATGTTACTGCTGCTGTTGGAGTACAACT
TCCCTATAGAAAACAACTGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAACTTAAAC
CCGAAGAAATTAGCATTCATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCAT
AGCAGTTCCAGATAAAAACTACATACGCCCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCT
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGGTCTCTAAAGGGGAGTTTTGTCTCTAC
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCT
GGCTGCCCAAAGGAATCAGCACGCCGGCCCTTCATCTTTTATAGGGCTCAGGTGGGCTCCTGGA
ACATGCTGGAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCT
GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTGAATTTTCATTTCAACCAGTTTGCAA
AGCTGAAATGAGCCCCAGTGAGGTCAGCGATTAGGAAACTGCCCCATTGAACGCCTTCCTCGCTA
ATTTGAACTAATTGTATAAAAACACCAAACCTGCTCACT

FIGURE 142

MLLLLLLEYNFIENNCQHLKTTHTFRVKNLNPKKFSIHDQDHKVLVLD SGNLI AVDPKNYIRPEI
FFALASSLSSASA EKGSPI LLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFI
FYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 33-36

N-myristoylation site.

amino acids 50-55, 87-92

Interleukin-1

amino acids 37-182

FIGURE 143

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTTAA
TCCAGGATCCTGTCTTCCTGTCTGTAGGAGTGCCTGTTGCCAGTGTGGGGTGAGACAAGTTTG
TCCCACAGGGCTGTCTGAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAACCTCCTGTGGG
CACGGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCATGCTGGGCCTGCCGTGG
AAGGGAGGTCTGTCTGGGCGCTGTGCTGCTTCTCTTAGGCTCCCAGATCCTGCTGATCTATGC
CTGGCATTTCACGAGCAAAGGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA
CAGTGGAGTTTGCTGTCCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGGG
CACATCTTGAATTCCCTGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT
GGGGAGAACTAGGTGTGGGAAATTTGAAGACGACATTGACAACCTGCCATTTCCAAGAAAGCACAG
AGCTGAACAATACTTTTACCTGCTTCTTCACCATCAGCACCAGGCCCTGGATGACTCAGTTCAGC
CTCCTGAACAAGACCTGCTTGGAGGGATTCCACTGAGTGAAACCCACTCACAGGCTTGTCATGT
GCTGCTCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTTCAGTGGCTGAGCAGCT
TTGGACTTGTTTGTATCCTATTTTGCATGTGTTTGAGATCTCAGATCAGTGTTTTAGAAAATCC
ACACATCTTGAGCCTAATCATGTAGTGTAGATCATTAAACATCAGCATTTTAAGAAAAAAAAAAAA
AA

FIGURE 144

MLGLPWKGGLSWALLLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY
YAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNTFTCFFTISTRP
WMTQFSLLNKTCLGFH

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 117-121, 139-143

N-myristoylation site.

amino acids 9-15

FIGURE 145

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCGATGAGGAAG
CACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCCGTCCA
GACGAGGGGCATCAAGCACAGAATCAAGTGGAACCGGAAGGCCCTGCCCAGCACTGCCCAGATCA
CTGAGGCCCAGGTGGCTGAGAACCGCCCGGAGCCTTCATCAAGCAAGGCCGCAAGCTCGACATT
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCGATGGCATCCA
CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTACCGGCTGCATCAATGCCA
CCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGGAGAGGGGCGCAGGACT
TCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGATCTGGCTCATGGTGAAAT
AAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAATCCTGGCAAGTGACCCAGCT
CTTCTCCCCCAAACCCACGCGTGTCTGAAGGTGCCAGGAGCGGCGATGCACTCGCACTGCAAA
TGCCGCTCCACGTATGCGCCCTGGTATGTGCCTGCGTTCTGATAGATGGGGGACTGTGGCTTCT
CCGTCACTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT
GAGAAGAACACATCAGGCACTGCGCCACCTGCTTCACAGTACTTCCCAACAACCTCTTAGAGGTAG
GTGTATTCCCGTTTTTACAGATAAGGAAACTGAGGCCAGAGAGCTGAAGTACTGCACCCAGCATC
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCTGGCTTGCTAACCAGGTTTTCTGCTCT
GTCCAATTCCAGAGCTGTCTGGTGATCACTTTATGTCTCACAGGGACCCACATCCAAACATGTAT
CTCTAATGAAATTGTGAAAGCTCCATGTTTAGAAATAAATGAAAACACCTGA

FIGURE 146

MRKHLSWWLATVCMLLFSLHSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNKLHQQ
VLWRLVQELCSLKHCFWLERGAGLRVTMHQPVLLCLLALIWMVK

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 157-171

N-glycosylation sites.

amino acids 98-102, 110-114

Tyrosine kinase phosphorylation site.

amino acids 76-83

N-myristoylation sites.

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

Amidation site.

amino acids 62-66

FIGURE 147

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCATT
CCTGATGATTTATAGACTCAAAGAAAACTATGTTCAGAAGCTCTCTTCTCTTCTGGCCTCCTCT
CTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG
AAATCTTTCATTTTGCTTGTCAGTGGGGTAGGTCAGTCTTAGTTTTATTTTTGAAATTT
CAACTTTCAGATTCAGGGGGTACATGTGAAGTTTGTTTTATGAGTATATTGCATTGATGCTGAGG
TTTGGGGT

FIGURE 148

MFRSSLLFWPPLCLLSLELLILISSIYSESKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE
GLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

FIGURE 149

GTCTCCGCGTCACAGGAACTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGACTTGAC
TCCCGCGCGCCCCAACCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGCCGCCAGTCC
CGGCCCCCTCTCCGCCCCACACCCACCCTCCTGGCTCTTCTGTTTTACTCCTCCTTTTCATTCTATA
ACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCAAGCCGAGCGTGGAAGAATGGGGTT
CCTCGGGACCGGCACTTGGATTCTGGTGTTAGTGCTCCCGATTCAAGCTTTCCCAAACCTGGAGGAA
GCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAA
GCAGAAGAAGACAAGATTAAAAAACATATCCTCCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTT
TGTTGATAACTTGAACCTGCTAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTA
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAATG
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCA
TCAACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAG
AAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAAACTACTTAATCTCGGCCTTATCACAGAAAGC
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCTCAAAGGAAGCCAACAA
TTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAG
TGACTCCAATGGCGCAATTCAAGATGGTCTTGCTAAGGGAGAAAACGATGAAACAGTATCTAACACA
TTAACCTTGACAAATGGCTTGGAAGGAGAACTAAAACCTACAGTGAAGACAACCTTTGAGGAACTCCA
ATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTTCAGAAAAAGAAGCAAAAGAGAAAGAAA
CACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCT
CCAGAAGAAGGTGTTTCTACCTTGAAAACCTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCT
AGAAAAAATGCTACTGACAATATAAGCAAGCTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAA
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCACAAAA
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGC
CATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGAAGATTATGACCTTT
CAAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAA
GAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAATGGCAAAGATCCAGGAGTCTTTCAA
CTGTTTCAGAAAACATAATATAGCTTAAACACTTCTAATCTGTGATTAAAAATTTTTGACCCAAGG
GTTATTAGAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCC
GTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 150

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG
QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK
FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAE
VLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVT PMAAIQDGLAKGENDET VSNLTLTNGLE
RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISP EEGV
SYLENLDEMIALQTKNLEKNATDNISKLF PAPSEKSHEETDSTKEEAAKMEKEYGSLKDSTKDD
NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLSKMRDFINKQADAYVEKGILDK
EEAEA IKRIYSSL

N-glycosylation sites:

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-
341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244

FIGURE 151

CGGCTCGAGGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCTGTGGAGCTCAA
GATGGTCTCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC
ATAATAACAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGC
GTGGTCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCCAGGGTGAAG
CCAGTGCCTGTCTGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG
AGCTCTATCTTGGTGCCAAGGAATCCAAGAGCTTACCTTCTACCGGCGGGACATGGGGCTCACC
TCCAGCTTCGAGTCGGCTGCCTACCCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCC
TGTCAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCATCACAGACTTCTACTTCC
AGCAGTGTGACTAGGGCAACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGTAGGGGT
GAGTGGAGGAGACCCATGGCGGACATCACTCTCTGTCTCTCAGGACCCCCACGTCTGACTTAG
TGGGCACCTGACCCTTTGTCTTCTGGTTCCTCAGTTTGGATAAATCTGAGATTTGGAGCTCAGT
CCACGGTCTCCCCACTGGATGGTGTCTACTGCTGTGGAACCTTGTA AAAACCATGTGGGGTAAA
CTGGGAATAACATGAAAAGATTTCTGTGGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCTGTCT
TAATGGTAACTGACAAAGTGTACCCCTGAGCCCCGAGGCCAACCCTCCCCAGTTGAGCCTTATA
GGGTCTAGTCTCTCCACATGAAGTCTGTCACTCACCCTGTGCAGGAGAGGGAGGTGGTCATA
GAGTCAGGGATCTATGGCCCTTGGCCAGCCCCACCCCTTCCCTTTAATCTGCCACTGTCTATA
TGCTACCTTTCCTATCTCTTCCCTCATCATCTTGTGTGGGCATGAGGAGGTGGTGTGTGAGAA
GAAATGGCTCGAGCTCAGAAGATAAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAA
GATACAATCAAAATCCAGATGCTGGTCTCTATTTCCCATGAAAAGTGCTCATGACATATTGAGA
AGACCTACTTACAAAAGTGGCATATATTGCAATTTATTTTAAATTAAGATAACCTATTTATATATT
TCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTGAGGGTGGTGGCAGTAT
AGGTGATTTTCTTTTAAATCTGTTAATTTATCTGTATTTCTTAATTTTCTACAATGAAGATGA
ATTCTTTGTATAAAAAAAGAAAAGAAATTAATCTTGAGGTAAGCAGAGCAGACATCATCTCTGA
TTGTCTCTCAGCCTCCACTTCCCCAGAGTAAATTCAAATTGAATCGAGCTCTGCTGCTCTGGTTGG
TTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGT
GTGGCTGGAATCTCTGGGTAAAGAACTTAAAGAACAAAAATCATCTGGTAATTCTTTCTAGAA
GATCACAGCCCCCTGGGATTCCAAGGCATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGA
ATTGTGTCCCCCTCAAATTCACATCCTTCTTGGAACTCTCAGTCTGTGAGTTTATTTGGAGATAAG
GTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCTATGCTGGATGAAGGTAGACCTAAATTCATAT
GACTGGTTTCTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA
AAGATGAAGGCAGAGATCGGAGTTTTCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACC
ATCAGAAGCTTGGAAGAGGCAAAGAAGAAATCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTG
CTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAAGAAATAAATTCGGCTGTTTTAA
GCCACCAAGGATAAATGGTTACAGCAGCTCTAGGAACTAATACAGCTGCTAAAATGATCCCTGT
CTCCTCGTGTTTACATTCTGTGTGTGTGCCCTCCCAATGTACCAAAGTTGTCTTTGTGACCAA
TAGAATATGGCAGAAAGTATGGCATGCCACTTCCAAGATTAGGTTATAAAAGACACTGCAGCTTC
TACTTGAGCCCTCTCTCTCTGCCACCCACCGCCCCAATCTATCTTGGCTCACTCGCTCTGGGGG
AAGCTAGCTGCCATGCTATGAGCAGGCCTATAAAGAGACTTACGTGGTAAAAATGAAGTCTCCT
GCCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTT
AAGTTGCTCAGTTTTGGTCTAACTTGTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG

FIGURE 152

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEIISVVPNRWLDASLSPVILGVQGG
QCLSCGVGQEPTLTLEPVNIMELYLGAKESKSTTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP
VRLTQLPENGAWNAPITDFYFQQCD

N-myristoylation sites.

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

Interleukin-1 signature.

amino acids 111-131

Interleukin-1 proteins.

amino acids 8-29, 83-120, 95-134, 64-103

FIGURE 153

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGGCCGC
CCTGCAGAAATCTGTGAGCTCTTTCCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTCTCTTGG
CCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAAC
TTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA
CAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT
ATCTGATGAAGCAGGTGCTGAACCTCACCCCTGAAGAAGTGCTGTTCCCTCAATCTGATAGGTTT
CAGCCTTATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGC
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTGCTGTTTATGTCTCTGAGAAAT
GCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTTCCCTGCTAGAAATAA
CAATTAGATGCCCCAAAGCGATTTTTTTTAAACAAAAGGAAGATGGGAAGCCAACTCCATCATG
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTTGTTTATA
AGACCAGAAGGTAGACTTTCTAAGCATAGATATTTATTGATAACATTTTCATTGTAAGTGGTGTTT
TATACACAGAAAACAATTTATTTTTTAAATAATTGTCTTTTCCATAAAAAAGATTACTTTCCAT
TCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAA
TGTATTTATTATTATTATAAGACTGCATTTTATTATATCATTTTATTAATATGGATTTATTTAT
AGAAACATCATTCGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTAT
AGAGCTATAACATGTTTATTTGACCTCAATAAACACTTGGATATCCC

FIGURE 154

MAALQKSVSSFLMGTLATSCLLLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL
ADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLFPQSDRFQPYMQEVVPFLARLSNRLS
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

[illegible][illegible]

FIGURE 156

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHYSHWPSCCPSKGQDTSEELLRWSTVPVPPLEPA
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS
ELLYHNQTVFYRRPCHGEKGTGTHKGYCLERRLYRVSLACVCVRPRVMG

Important features of the protein:

Signal peptide:

amino acids 1-32

N-glycosylation site.

amino acids 136-140

Tyrosine kinase phosphorylation site.

amino acids 127-135

N-myristoylation sites.

amino acids 44-50, 150-156

FIGURE 157

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCC
GACCGTTCAATGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCC
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACAGTGTGCAACAGGGGACTATTCA
ATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGAAGGCCACCAA
GATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTACAGCTGTGTGAGGTGCAATTACACAGAGG
CCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCTACATCGGCTTCCCTGTA
GAGCTGAACACAGTCTATTTTATTGGGGCCATAATATTCTAATGCAAATATGAATGAAGATGG
CCCTTCCATGTCTGTGAATTTTACCTCACCAGGTGCCTAGACCACATAATGAAATATAAAAAA
AGTGTGTCAAGGCCGAAGCCTGTGGGATCCGAACATCACTGCTTGTGAAGAAGATGAGGAGACA
GTAGAAGTGAACCTTACAACCACTCCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCAC
TATCATCGGGTTTTTCTCAGGTGTTTGGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGA
TTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGC
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCT
GGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCA
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTT
TCTACCACCACACTACTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCA
TCACACAATTTGTTACTTCACTGAATTTCTTCAAAACCATTGCAGAAGTGAGGTCATCCTTGAAA
AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCA
GCAGACAAAGTCGTCTTCCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAA
GAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCTTTAACCTTTTCTGCA
GTGATCTAAGAAGCCAGATTCTCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACA
AAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT
CTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTGAGCAGGAAAAAGATCACAAGCCTGCCACG
ATGGCTGCTGCTCCTTGTAG

FIGURE 158

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPDGLRDLRVEPVTTSVATGDYSILMNVSWV
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVEINTVYFIGAHNIP
NANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQH
STIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPTGVPFPLDNNK
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFL
QNHCRSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHVKQQVSAGKRSQACHD
GCCSL

Important features of the protein:

Signal peptide:

amino acids 1-14

Transmembrane domain:

amino acids 290-309

N-glycosylation sites.

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283
- 287

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 228 - 232 and 319 - 323

Casein kinase II phosphorylation sites.

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

N-myristoylation site.

amino acids 116-122

Amidation site.

amino acids 488-452

FIGURE 159

AGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCATGGTCAAGTACTTGCTGCT
GTCGATATTGGGGCTTGCCTTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA
CTTTTTTCCAAAAGCCTGAGAGTTGCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC
ATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG
GAATTACACTGTCACCTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCCAGTGTAGGA
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAA
GAGACCCTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTTCTTTCCAGTTGGAGAAGGTGCT
GGTGACTGTTGGCTGCACCTGCGTCACCCCTGTCATCCACCATGTGCAGTTAAGAGGTGCATATCC
ACTCAGCTGAAGAAG

FIGURE 16o

MTVKTLHGPMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINEN
QRVSMsrNIESRSTSPWNYTWTWDPNRYPSVVQAQCRNLGCINAQKEDISMNSVPIQQETLVV
RRKHQGCsvSFQLEKVLVTVGCTCVTPVIHHVQ

Signal sequence:

amino acids 1-30

N-glycosylation site.

amino acids 83-87

N-myristoylation sites.

amino acids 106-111, 136-141

FIGURE 161

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCAGG
ACAGAGAGTGCACAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGGATTTC
CAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGCAGCAC
AGGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAGATGCCTGTGCCCTGGTTCTTGCTGTCT
TGGCACTGGGCCGAAGCCAGTGGTCTTTCTCTGGAGAGGCTTGTGGGGCCTCAGGACGCTACC
CACTGCTCTCCGGGCTCTCCTGCCGCTCTGGGACAGTGACATACTCTGCCCTGCCCTGGGGACAT
CGTGCCCTGCTCCGGGCCCCGTGCTGGCGCCTACGCACCTGCAGACAGAGCTGGTGCTGAGGTGCC
AGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGCCGTGCATGGGCACTGG
GAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAGGAA
TGCCTCTCTCCAGGCCAAGTCGTGCTCTCCTTCCAGGCCTACCTACTGCCCGCTGCGTCTGCTG
TGGAGGTGCAAGTGCCCTGCTGCCCTTGTGCACTTGGTTCAGTCTGTGGGCTCTGTGGTATATGAC
TGCTTCGAGGCTGCCCTAGGGAGTGAAGTACGAATCTGGTCTTACTCAGCCAGGTACGAGAA
GGAATCAACACACACAGCAGCTGCCCTGCCCTGGCTCAACGTGTGACGAGATGGTGACA
ACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCACTTCGGCCTCTCCCTGTACTGGAATCAG
GTCCAGGGCCCCCAAAACCCCGGTGGCACAAAACCTGACTGGACCGCAGATCATTACCTTGAA
CCACACAGACCTGGTTCCTGCTCTGTATTAGGTGTGGCCTCTGGAACCTGACTCCGTTAGGA
CGAACATCTGCCCTTCAGGGAGGACCCCGCGCACACCAGAACCTCTGGCAAGCCGCCCGACTG
CGACTGTGACCTGCAGAGCTGGGTGCTGGACGCAACCGTGTCTGCTGCCCGCAGAAGCGGCACT
GTGCTGGCGGGCTCCGGGTGGGGACCCCTGCCAGCCTGGTCCCACCGCTTTCCTGGGAGAACG
TCACTGTGGACAAGGTTCTCGAGTTCCCATTTGCTGAAAGGCCACCTAACCTCTGTGTTTCAGGTG
AACAGCTCGGAGAAGCTGCAGCTGCAGGAGTGTCTGTGGGCTGACTCCCTGGGGCCTCTCAAAGA
CGATGTGCTACTGTTGGAGACACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTTGGAAACCA
GTGGCTGTACTTCACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTACTA
CAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTG
CCCCATGGACAAATACATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCTACTCTTTGCCG
CTGCGCTTTCCCTCATCTCTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAGGCTCTTGA
CAGGACGTCCGCTCGGGGGCGGCCGCCAGGGGCCGCGCGGCTCTGCTCCTCTACTCAGCCGATGA
CTCGGGTTTCGAGCGCCTGGTGGGGCGCCCTGGCGTGGGCCCTGTGCCAGCTGCCGCTGCCGCTGG
CCGTAGACCTGTGGAGCCGTCTGTAACTGAGCGCGCAGGGGCCGTGGCTTGGTTTCACGCGCAG
CGGCGCCAGACCTGCAGGAGGGCGCGGTGGTGGTCTTGTCTCTCTCCCGGTGCGGTGGCGCT
GTGCAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCGGGCGCACGGCCCGCACGACGCTTCC
GCGCCTCGCTCAGCTGCGTGTGCCGACTTCTTGACGGGCCGGGGCGCCCGGACGTACGTGGGG
GCCTGCTTCGACAGGCTGTCTCACCAGGACGCCGTACCCGCCCTTTTCCGACCGGTGCCCGTCTT
CACACTGCCCTCCCACTGCCAGACTTCTGGGGGCCCTGCAGCAGCCTCGCGCCCCGCGTTCCG
GGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCAGCCAGCCCTGGATAGCTACTTC
CATCCCCCGGGGACTCCCGCGCGGACGCGGGTGGGACCAGGGGCGGGACCTGGGGCGGGGA
CGGGACTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAA

FIGURE 162

MPVPWFLLSLALGRSPVVLSELRLVGPQDATHCSPGLSCRLWSDILCLPGDIVPAPGPVLAPTHLQTELV
LRCQKETDCDCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSTQAYPTARCVLLEV
QVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVNSADGDNVHLVLNV
EEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQ
LWQAARLRLTLQSWLLDAPCSLPAAEALCWRAPGGDPCQPLVPLSWENVTVDKVLEFPLLKGHPNLCVQ
VNSSEKLQEQECLWADSLGPLKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRAARLGEYLLQDLQS
GQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSILLKLDHAKGWLRLKQDVRSGAAARG
RAALLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAFHQAQRQTLEGGVVVLLFSP
GAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFT
LPSQLPDLFGALQQPRAPRSRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

Signal sequence:

amino acids 1-20

Transmembrane domain.

amino acids 453-475

N-glycosylation sites.

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,
334-337, 357-360, 391-394

Glycosaminoglycan attachment site.

amino acids 583-586

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 552-555

N-myristoylation sites.

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,
692-697, 696-701, 700-705

FIGURE 163

GGGAGGGCTCTGTGCCAGCCCCGATGAGGACGCTGCTGACCATCTTGACTGTGGGATCCCTGGCT
GCTCACGCCCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCAGTCCAGCAACTTTGA
AAACATCCTGACGTGGGACAGCGGGCCAGAGGGCACCCAGACACGGTCTACAGCATCGAGTATA
AGACGTACGGAGAGAGGGACTGGGTGGCAAAGAAGGGCTGTCAGCGGATCACCCGGAAGTCTGTC
AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTCACCGCT
GTCAGTGGGGAGGGCCGGTCAGCCACCAAGATGACTGACAGGTTACAGTCTCTGTCAGCACACTAC
CCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAGATCGATTAGATGATTGTTTCATCCTA
CCCCACGCCAATCCGTGTCAGGCGATGGCCACCGCTAACCCCTGGAAGACATCTTCCATGACCTG
TTCTACCACTTAGAGCTCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGGAAGCAGAGAGA
ATATGAGTTCTTCGGCTGACCCCTGACACAGAGTTCTTGGCACCATCATGATTTGCGTTCCCA
CCTGGGCCAAGGAGAGTGGCCCCCTACATGTGCCGAGTGAAGACACTGCCAGACCGGACATGGACC
TACTCCTTCTCCGGAGCCTTCTGTCTCCATGGGCTTCTCGTCGAGTACTCTGCTACCTGAG
CTACAGATATGTCACCAAGCCGCTGACCTCCCAACTCCCTGAACGTCCAGCGAGTCTGACTT
TCCAGCCGCTGCGCTTTCATCCAGGAGCACGTCCCTGATCCCTGTCTTGACCTCAGCGGCCAGC
AGTCTGGCCAGCCTGTCCAGTACTCCAGATCAGGGTGTCTGGACCCAGGGAGCCCGCAGGAGC
TCCACAGCGGCATAGCCTGTCCGAGATCACTACTTAGGGCAGCCAGACATCTCCATCCTCCAGC
CCTCCAACGTGCCACCTCCCCAGATCCTCTCCCCACTGTCTATGCCCCAAACGCTGCCCTGAG
GTCGGGCCCCCATCCTATGCACCTCAGGTGACCCCCGAAGCTCAATTCCCATTCTACGCCCCACA
GGCCATCTTAAGGTCAGCCTTCTCTATGCCCTCAAGCCACTCCGGACAGCTGGCCTCCCT
CCTATGGGGTATGCATGGAAGTTCTGGCAAAGACTCCCCACTGGGACACTTTCTAGTCTTAA
CACCTTAGGCCTAAAGGTCAGCTTTCAGAAAGAGCCACCAGCTGGAAGCTGCATGTTAGGTGGCCT
TTCTCTGCAGGAGGTGACCTCCTTGCTATGGAGGAATCCCAAGAAGCAAAATCATTGCACCAGC
CCCTGGGGATTTCACAGACAGAACATCTGACCCAAATGTGCTACACAGTGGGGAGGAAGGGACA
CCACAGTACCTAAAGGGCCAGCTCCCCCTCCTCTCCTCAGTCCAGATCGAGGGCCACCCCATGTC
CCTCCCTTTGCAACCTCCTTCCGGTCCATGTTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGGCC
TGCTGGAGTCCCTTGTGTGTCCCAAGGATGAAGCCAAGAGCCAGCCCCTGAGACCTCAGACCTG
GAGCAGCCACAGAACTGGATTCTCTTTTCAGAGGCTGGCCCTGACTGTGTCAGTGGGAGTCC**TG**
AGGGGAATGGGAAAGGCTTGGTGCTTCTCCCTGTCCCTACCCAGTGTACATCCTTGGCTGTCA
ATCCCATGCCTGCCATGCCACACACTCTGCGATCTGGCCTCAGACGGGTGCCCTTGAGAGAAGC
AGAGGGAGTGGCATGCAGGGCCCCCTGCCATGGGTGCGCTCCTCACCGGAACAAAGCAGCATGATA
AGGACTGCAGCGGGGGAGCTCTGGGGAGCAGCTTGTGTAGACAAGCGCGTGTCTGAGCCCTG
CAAGGCAGAAATGACAGTGCAAGGAGGAAATGCAGGGAACTCCCGAGGTCCAGAGCCCCACCTC
CTAACACCATGGATTCAAGTGCTCAGGGAATTTGCCCTCCTTGCCCCATTCTGGCCAGTTTC
ACAATCTAGCTCGACAGAGCATGAGGCCCTGCCCTTCTGTCTATTGTTCAAAGGTGGGAAGAGA
GCCTGGAAAAGAACCAGGCCTGGAAAAGAACCAGAAGGAGGCTGGGCAGAACCAGAACAACCTGC
ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCCTGCAGCTCA
TTCCAGCCAGGGCAACTGCCTGACGTTGCACGATTTAGCTTCATTCCTCTGATAGAACAAGC
GAAATGCAGGTCCACCAGGGAGGGAGACACACAAGCCTTTCTGCAGGCAGGAGTTTCAGACCT
ATCTGAGAATGGGGTTTGAAGGAAGGTGAGGGCTGTGGCCCTGGACGGGTACAATAACACAC
TGTAATGATGTACAACCTTTCAGGCTCTGCCTTGGGTTTCAGCCCATCTGGGCTCAAATTCAGC
CTCACCCTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCCAGAACCTCGGTTTCTC
ATCTGTAATGTGGGGATCATAACACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGTCATG
TCTTTAAAGTGCTTAATAGTGCTTGGTACATGGGCAGTGCCCAATAAACGGTAGCTATTTAAAA
AAAAAAA

FIGURE 164

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTVYSIEYKTYGERDW
VAKKGCQRITRKSCNLTIVETGNLTelyarvtavsaggrsatkmtDRFSSLQHTTLKPPDVCIS
KVRSIQMIHVHTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRTYQMHGGKQREYEFFGLTPDT
EFLGTIMICVPTWAKESAPYMCrvKTLpDRTWTYSFSGAFLFSMGFLVAVLCYLSYRYVTKPPAP
PNSLNVQRVLTfQPLRFIQEHVLIpVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT
YLGQPDISILQPSNVPPPQILSPLSYAPNAapevgPPSYAPQVTPEAQFPFYAPQAISKVQPSSY
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPKGQLQKEPPAGSCMLGGLSLQEVTSLAM
EESQEAksLHQPLGICTDRtSDPNVLHSGEEGTPQYLKGQLPLLSSVQIEGHpMSLPLQPPSGPC
SPSDQGpSPWGLLESLVCPKDEAKSPAPETSDLEQPTELDSLFRGLALTvQWES

Signal sequence.

amino acids 1-17

Transmembrane domain.

amino acids 233-250

N-glycosylation sites.

amino acids 80-83, 87-90, 172-175

N-myristoylation sites.

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

FIGURE 165

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGGTGGCCACAACATGG
CTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTCTGTGCTGGGGGCGCTCTGGTGGGTCCCGGGCCAG
TCGGATCTCAGCCACGGACGGCGTTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTGCAGCAT
GTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGTGAATTTTA
AAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAACCTTGGGCTGGA
AGTGTTGAACACAGTTTTGGATATTTTCCAAAAGATTTGATCAAGGTACTTCATAAATACACGGA
AGAAGAGCTACATATTCAGCAGATGAGACAGACTTTGTCTGCTTGAAGGAGGAAGAGATGATT
TTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAAGTGGAGGACTCTGTACCTGAAGAG
TCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGGCGTGA
ACTTGACCCTGTGCCTGAGCCCCGAGGCATTTCAGAGCTGATTTCAGAGGATGGAGAAGGTGCTTCT
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCTCACACCAGCGGT
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACACTTTTGAAGAAATTCTGCACGATAA
ATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGGTGGAGCGGGAGA
AGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGCCTTATT
CATTACAGCAAAGGATTTTCGTTGGCATCAAATCTAAGTTTGTGTTTACAAAGATTGTTTTTTAGTA
CTAAGCTGCCTTGGCAGTTTGCATTTTTGAGCCAAACAAAATATATTATTTCCCTTCTAAGTA
AAAAAAAAAAAAAAAAAAAA

FIGURE 166

MAAAPGLLFWLFVLGALWWVPGQSDLSHGRRFSDLKVCGDEECSMLMYRGKALEDFTGPDCRFVN
FKKGDDVYVYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEELHIPAETDFVCFEGGRD
DFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPEESRGRELDPVPEPEAFRA SEDGE GA
FSESTEG LQGQPSAQESH PHTSGPAANAQGVQSSLDTFEEILHDKLVPGSESRTGNSSPASVER
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNL SLFYKDCF

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 294-298

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34

Tyrosine kinase phosphorylation site.

amino acids 67-76

N-myristoylation sites.

amino acids 205-211, 225-231, 277-283

Amidation site.

amino acids 28-32

FIGURE 167

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTTCAGAGGCCGGGGAAGAGAAGCAAAGCGC
AACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCCTAACTTC
AGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCGCGGCACAGG
CGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAGCTGGGCTCGGGC
GGCGGGAGTAGGGCCCGGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTCGCGGGCTGCGCCCTG
GGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGATGAGCCGCGTGG
TCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCCGCCGCGTGGTCAGC
GGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCCTACTTCCATGAACT
GTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTTGTGAGAGTGAGGGAGGAGTCCTCCTCA
GCCTTGAGAAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGCAAAAACCTGACAAAACCCGGG
ACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGAATGGAGATGGGCAAACATCTGG
TGCCTGCCCAGATCTCTACCAGTGGTCTGATGGAAGCAATCCCAGTACCGAAACTGGTACACAG
ATGAACCTTCCTGCGGAAGTGAAAAGTGTGTTGTGATGTATCACCAACCAACTGCCAATCCTGGC
CTTGGGGGTCCCTACCTTTACCAGTGAATGATGACAGGTGTAACATGAAGCACAATTATATTTG
CAAGTATGAACCAGAGATTAATCCAACAGCCCCTGTAGAAAAGCCTTATCTTACAAATCAACCAG
GAGACACCCATCAGAATGTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTT
ATACCAACAATACCCCTGCTCTTACTGATACTGGTTGCTTTTGGAACTGTTGTTTCCAGATGCT
GCATAAAAGTAAAGGAAGAACAACAACTAGTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTA
CCAGAAAAGAAAGTGGCATGGAAGTATAATAACTCATTGACTTGGTTCCAGAATTTTGTAATTCT
GGATCTGTATAAGGAATGGCATCAGAACAATAGCTTGAATGGCTTGAAATCACAAAGGATCTGC
AAGATGAACTGTAAGCTCCCCCTTGAGGCAAATATTAAAGTAATTTTTTATATGTCTATTATTTCA
TTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGTCTAAAGGATGCACCCAA
ACTTCAAACCTTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTA
TGTGTGTTAGAAAGCAATTCCTTTTATTTCTTTCACCTTTCATAAGTTGTTATCTAGTCAATGTAA
TGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGGTTGATAAAA
ATGAACTGTTCTAATATTTATTTTATGGCATCTCATTTTCAATACATGCTCTTTTGATTAAAG
AACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTTGT
TTTCTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTTCAGA
AATAAGAAGCTATTTTCATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGAT
TGTCTAATTTCAATTGTGCAAGACATGTGCCTTATAATTATTTTGTCTTAAATTAACAGATT
TTGTAATAATGTAACCTTGTTAATAGGTGCATAAACACTAATGCAGTCAATTTGAAQAAAAGAAG
TGACATACACAATATAAATCATATGTCTTCACACGTTGCCTATATAATGAGAAGCAGCTCTCTGA
GGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTCTGGGGTTTGGG
ATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTG
ACTATATTAGTATACAAAGAGGTGATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAG
ACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACACGAAATCGTGTGAAAATGGGTTGG
AACCCATCAGTGATCGCATATTCATTGATGAGGGTTTGGCTTGGATAGAAAATGGTGGCTCCTTT
CTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTCTCTCAAGAGAAAGTTGTAACCTCT
CTGGTCTTCATATGTCCCTGTGCTCCTTTTAACCAATAAAGAGTTCTTGTCTTGGGGGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 168

MSRVVSLLLGAALLCGHGAFCRRVVSQGKVCFADFKHPCYKMAYFHELSSRVSFQEARLACESE
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDGFWIGLWRNGDGQTSGACPDLYQWSDGSNSQ
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAPVEK
PYLTNQPGDTHQNVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKS KGRTKTSPNQ
STLWISKSTRKESGMEV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89, 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145, 212-217